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Requester's Full Name: Myron Hill Examiner #: 78884 Date: 11/4/03
 Art Unit: 1648 Phone Number 30 84521 Serial Number: 09/830 981
 Mail Box and Bldg/Room Location: 8E17 Results Format Preferred (circle): PAPER DISK E-MAIL
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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Cell Permeability Modulating Peptide

Inventors (please provide full names): 1) Hill, Myron
2) Oess (Geb. Schmidt), Stephanie

Earliest Priority Filing Date: 11/3/98 Schmitt

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

C. Chan
Rush

Please STN formula of claim 1. and

2) STN seq. of Fig. 1 which is: SEPIO^{#2}

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AA 12

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Type of Search

Vendors and cost where applicable

Searcher: Bachly 24999 NA Sequence (#) STN
 Searcher Phone #: AA Sequence (#) Dialog
 Searcher Location: Structure (#) Questel/Orbit
 Date Searcher Picked Up: Bibliographic Dr. Link
 Date Completed: 11-07-03 Litigation Lexis/Nexis
 Searcher Prep & Review Time: 20 Fulltext Sequence Systems
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 Online Time: 33 Other Other (specify) CGN

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OM protein - protein search, using sw model

Run on: November 6, 2003, 15:02:33 ; Search time 41 Seconds

(without alignments)
46.457 Million cell updates/sec

Title: US-09-830-981-2

Perfect score: 61

Sequence: 1 PLSIFSRIGDP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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23: /SIDS1/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	12	21	AA10598
2	61	100.0	12	21	AA10598
3	61	100.0	12	23	ABG78991
4	61	100.0	25	12	AA14747
5	61	100.0	36	23	AA17023
6	61	100.0	60	16	AA176747
7	61	100.0	102	20	AA130947
8	61	100.0	164	21	AA13740
9	61	100.0	164	21	AA190760

10	61	100.0	174	12	AA15617
11	61	100.0	174	13	AA123867
12	61	100.0	215	21	AA10597
13	61	100.0	281	13	AA127471
14	61	100.0	281	20	AA132835
15	61	100.0	389	13	AA127472
16	61	100.0	389	13	AA127474
17	61	100.0	393	22	AA14097
18	59	96.7	55	8	AA170002
19	59	96.7	64	22	AA181133
20	59	96.7	64	23	AA17027
21	59	96.7	67	22	AA181135
22	59	96.7	67	23	AA17029
23	59	96.7	174	12	AA15618
24	59	96.7	174	13	AA123868
25	59	96.7	174	24	AA158074
26	59	96.7	347	21	AA10596
27	59	96.7	389	22	AA166931
28	59	96.7	389	24	AA155073
29	54	88.5	174	12	AA12394
30	54	88.5	174	12	AA15622
31	54	88.5	174	13	AA12871
32	54	88.5	174	24	AA158070
33	54	88.5	174	24	AA158071
34	54	88.5	174	24	AA158072
35	54	88.5	174	24	AA158073
36	54	88.5	281	7	AA160163
37	54	88.5	281	7	AA160560
38	54	88.5	281	7	AA160617
39	54	88.5	281	8	AA170294
40	54	88.5	281	15	AA162870
41	54	88.5	281	20	AA132834
42	54	88.5	281	22	AA164419
43	54	88.5	389	7	AA160794
44	54	88.5	400	17	AA193801
45	54	88.5	400	21	AA154045

ALIGNMENTS

RESULT 1	AA10598	AA10598
ID	AA10598	standard; Protein; 12 AA.
AC	AA10598;	
XX		
DT	08-JAN-2001	(first entry)
DE	HBV fusion protein cell permeability peptide fragment.	
XX		
KW	Fusion protein; protein coat; virus-specific packaging signal; psi;	
KW	virus protein; cell permeability; cell-specific binding site; LMB;	
KW	large surface protein; core antigen; gene therapy.	
OS	Hepatitis b virus.	
XX		
PN	WO200046376-A2.	
XX		
PD	10-AUG-2000.	
XX		
PF	04-FEB-2000; 2000MO-DE00363.	
XX		
PR	05-FEB-1999; 99DE-1004800.	
XX		
PA	(HILD/) HILD E.	
XX		
PI	Hildt E, Hofecheider P;	
XX		
DR	WPI; 2000-514959/46.	
XX		
DR	N-PSDB; AA17151.	
XX		
PT	Particle for cell-specific gene delivery, useful in gene therapy.	

PT comprises nucleic acid in protein coat that includes a fusion protein
XX of viral protein, permeability peptide and cell-binding site -
PS Disclosure; Page 2; 34pp; German.

XX This invention describes a novel particle (A), comprising a protein coat
CC with a fusion protein (FP), and, inside the coat, a nucleic acid (I)
CC including the sequence for a virus-specific packaging signal (psi) and a
CC structural gene. FP contains a virus protein (VP), a peptide (P) that
CC mediates cell permeability and a heterologous cell-specific binding site
CC (RGD). The invention also describes (1) producing (A) in which FP
CC contains an LHBs (large surface protein of hepatitis B virus (HBV)) and
CC RGD; (2) preparing (A) in which FP contains an HBV core antigen (HBCag),
CC (P) and RGD; (3) FP; (4) DNA encoding FP; and (5) expression vector
CC containing the DNA of (d). The products of the invention are used in gene
CC therapy of cells and tissues, in vivo or ex vivo. This sequence
CC represents a fragment of the Hepatitis B virus cell permeability peptide
CC which is described in the method of the invention.

XX Sequence 12 AA;

Query Match 100.0%; Score 61; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
1 PLSSTFSRIGDP 12

DB 1 PLSSTFSRIGDP 12
RESULT 2
AA87906
ID AAY87906 standard; Protein; 12 AA.

XX AAY87906;

XX 01-SEP-2000 (first entry)

XX HBV cell surface protein ZPP fragment.

XX Cell surface protein; ZPP, cell permeability mediating polypeptide;

XX therapy; treatment.

XX Hepatitis B virus.

XX DE19850718-C1.

XX 18-MAY-2000.

XX 03-NOV-1998; 98DE-1050718.

XX 03-NOV-1998; 98DE-1050718.

XX (HILD/) HILD E.

XX Hildt E, Oess S;

XX WPI, 2000-340689/30.

XX N-PSDB; AAA95621.

PT Novel cell permeability-mediating polypeptide useful for mediating
PT permeability of substances such as other polypeptides in cells -

XX Claim 1; Fig 1; 8pp; German.

XX This invention describes a novel cell permeability mediating polypeptide
CC (CPM) comprising (A) or a sequence which differs by one or more amino
CC acids, which shows cell permeability and is not hepatitis B virus (HBV)
CC surface protein and where the DNA sequence of the latter amino acid
CC sequence hybridizes with the DNA of (I). CPM can be used to mediate cell
CC permeability of substances, especially polypeptides, nucleic acids and
CC chemical connections. This is useful for increasing the reactivity of
CC such substances in therapeutic treatment of various conditions. This

CC sequence represents a fragment of the HBV cell surface protein ZPP which
CC is described in the method of the invention.

XX Sequence 12 AA;

Query Match 100.0%; Score 61; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
1 PLSSTFSRIGDP 12

DB 1 PLSSTFSRIGDP 12
RESULT 3
ABG78991
ID ABG78991 standard; Peptide; 12 AA.

XX ABG78991;

XX 15-NOV-2002 (first entry)

XX Cell penetrating peptide PRES.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma;
XX Lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukemia;
XX Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
XX kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
XX ovarian cancer; pancreatic cancer; vaccine; dendritic cell;
XX tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
XX cytostatic.

XX Hepatitis B virus.

XX WO200264057-A2.

XX 22-AUG-2002.

XX 15-FEB-2002; 2002WO-US05212.

XX 15-FEB-2001; 2001US-268687P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;

XX WPI, 2002-627577/67.

XX Novel composition for treating a disease in an animal, comprises an
XX immune effector cell and cell penetrating peptide associated with an
XX antigen or antibody -

XX Disclosure; Page 11; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP
CC associated with an antigen, and a pharmaceutically acceptable carrier
CC and (2) preparing a composition for a disease, by providing (I)
CC and CPP associated with an antigen for disease, and introducing the
CC antigen-associated CPP to (I), where antigen enters into the cell.
CC The antigens are, for example, tumour antigen derived epitopes
CC recognised by tumour infiltrating lymphocytes (TIL) of HLA (human
CC leukocyte antigen) class I or II. The composition is useful for enhancing
CC immunity in an animal to a disease, by administering a mature dendritic
CC cell comprising CPP associated with an antigen to disease, to the animal,
CC such that following the administration, animal is protected from disease,
CC where the animal comprises both CD4+ and CD8+ T cells. It is also useful
CC for treating a disease (e.g. cancer, tumour, melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukemia,
CC Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer,
CC kidney cancer, adenocarcinoma, breast cancer, prostate cancer,
CC ovarian cancer and pancreatic cancer). The animal is further subjected to

CC a cancer treatment including surgery, radiation, chemotherapy or gene
CC therapy. The administration of (1), preferably dendritic cell is prior
CC to, subsequent to or concurrent with, the cancer treatment. The present
CC sequence is cell penetrating peptide of the invention.

XX Sequence 12 AA;

Query Match 100.0%; Score 61; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFSRIGDP 12
DB 1 PLSISFSRIGDP 12

RESULT 4

AAE14747 standard; peptide; 25 AA.

XX AAE14747;

AC 28-JAN-1992 (first entry)

XX HBV Pre S2 peptide.

DE Monoclonal antibodies; hepatitis B virus; envelope; vaccine;

XX epitope; antigen.

OS Synthetic.

XX EP456215-A.

XX 13-NOV-1991.

XX 08-MAY-1991; 91EP-0107488.

XX 11-MAY-1990; 90US-0522286.

XX (ABBO) ABBOTT LABORATORIES.

XX Mims LT, Floreani MF;

XX WPI; 1991-334198/46.

XX New MAb to Pres2 and Pres1 polypeptide(s) of Hepatitis-B

PT envelope - used to sub-type HBV in sample and as vaccine against

PT HBV.

PS Claim 1, Page 22; 24pp; English.

CC The peptide corresponds to residues 150-174 of the HBV Pres2 protein.

CC It was used to raise monoclonal antibodies specific for the HBV M

CC protein but which do not bind to the HBV S or L proteins. The MAb

CC can be used to sub-type HBV and to prepare subunit vaccines for HBV.

XX Sequence 25 AA;

Query Match 100.0%; Score 61; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFSRIGDP 12
DB 11 PLSISFSRIGDP 22

RESULT 5
AAE17023 standard; peptide; 36 AA.
XX AAE17023;
XX AAE17023;
XX

DT 18-APR-2002 (first entry)

DE Hepatitis B virus (HBV) ayw subtype pre-S2 region.

XX Hepatitis B virus; HBV, core antigen, HBcAg; immune system; typhoid;

XX prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes;

XX hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea;

XX tuberculosis; polio; rabies; acquired immunodeficiency syndrome; AIDS;

XX dengue fever; yellow fever; malaria; whooping cough; salmonellosis;

XX food poisoning; meningitis; gonorrhea; antiviral; antibacterial;

XX antiprotocozal; pre-S2 region.

XX Hepatitis B virus.

XX WO200198333-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-GB02817.

XX 22-JUN-2000; 2000GB-0015308.

XX 06-OCT-2000; 2000GB-0024544.

XX (CELL-) CELTECH PHARM LTD.

XX Page M, Li J, Pumpens P;

XX WPI: 2002-098223/13.

XX N-PsDB; AMD27424.

XX New proteins comprising a modified hepatitis B core antigen, useful as

XX a vaccine in prophylactic or therapeutic vaccination of the human or

XX animal body, particularly against hepatitis B virus infection -

XX Disclosure; Fig 3A; 40pp; English.

XX The invention relates to modified proteins comprising hepatitis B virus

XX (HBV) core antigen (HBcAg) wherein one or more of the four arginine

XX repeats has been deleted and the protein comprising the C-terminal

XX cysteine of HBcAg. The deleted region may be replaced by an epitope

XX from a protein other than HBcAg, in which case the HBcAg acts as a

XX carrier to present the epitope to the immune system. This chimeric

XX protein or its nucleic acid is useful as a vaccine or in a method of

XX prophylactic or therapeutic vaccination of the human or animal body,

XX particularly against HBV. The nucleic acid encoding the protein may

XX be used in gene therapy or DNA vaccination protocols. The chimeric

XX protein or its nucleic acid may also be used as the basis of a

XX prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis

XX A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth

XX disease, polio, herpes, rabies, acquired immunodeficiency syndrome

XX (AIDS), dengue fever, yellow fever, malaria, tuberculosis, whooping

XX cough, salmonellosis, typhoid, food poisoning, diarrhoea, meningitis

XX or gonorrhea. The present sequence is Hepatitis B virus (HBV) ayw

XX subtype pre-S2 region.

XX Sequence 36 AA;

Query Match 100.0%; Score 61; DB 23; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFSRIGDP 12
DB 22 PLSISFSRIGDP 33

RESULT 6
AAR76747 standard; peptide; 60 AA.
XX AAR76747;
XX AAR76747;
XX 18-MAR-1996 (first entry)

```

DE XX HBV surface antigen pre-S2 region and FimH residues 224-226.
XX
XX FimH; type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue;
XX FimA; FimF; FimG; receptor binding site; PCR; amplify.
XX
XX Chimeric - Hepatitis B virus.
OS Chimeric - Escherichia coli.
XX
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "Represents FimH residue 224"
FT Peptide 2..4 /note= "Linker peptide"
FT Peptide 5..56 /note= "HBV surface antigen pre-S2 region"
FT Peptide 57..59 /note= "Linker peptide"
FT Misc-difference 60 /note= "Represents FimH residue 226"
FT
XX
XX WO9520657-A1.
XX
XX 03-AUG-1995.
XX
XX 27-JAN-1995; 95WO-DK00042.
XX
XX 27-JAN-1994; 94US-0187166.
XX
XX (GXBI-) GX BIOSYSTEMS AS.
XX
XX Haery DL, Klemm P, Molin S, Pallesen L, Sokurenko EV;
XX
XX WPI; 1995-275442/36.
XX
XX N-PSDB; AAQ93059.
XX
XX Receptor specific bacterial adhesins - useful for targeting active
XX compounds and microbial cells to locations of receptors
XX
XX Example 3; Page 57; 152pp; English.
XX
XX This sequence is encoded by a fragment of the plasmid pLPA38, which
XX comprises a fimH fusion gene comprising the sequence encoding the pre-S2
XX region of the hepatitis B viral surface antigen inserted into the fimH
XX gene. The primer sequences given in AAQ93057-58 caused the insertion of
XX the pre-S2 region into the FimH protein at position 224-226. The
XX resulting chimeric gene was then further modified by insertion of the
XX cholera toxin B chain into a different position of the FimH adhesin of
XX type 1 fimbriae. Restriction site handles (tgII-sites) were introduced
XX into the FimH gene, and the foreign epitopes are then inserted in-frame.
XX In the selected positions the insertion of the epitopes did not
XX significantly alter the adhesive function of the FimH protein. The
XX expression of the chimeric proteins on the surface of fimbriae on
XX bacterial hosts illustrated the possibility of using bacterial adhesins
XX as general presenters of foreign antigens and epitopes. These chimeric
XX genes may be used in the production of variant FimH adhesins which may
XX be useful for targeting active compounds and microbial cells to
XX locations comprising selected receptors to which the adhesins bind.
XX
XX Sequence 60 AA:
XX
XX
XX Query Match 100.0%; Score 61; DB 16; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 0.00026;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 PLSSTFSRIGDP 12
XX |||||
XX 42 PLSSTFSRIGDP 53
XX
XX
XX RESULT 7
XX AAQ930947
XX
XX AAQ930947 standard; Protein; 102 AA.

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XX AY30947;
XX
XX 20-OCT-1999 (first entry)
XX
XX Human HbsAg (Pres2 plus S region) truncated peptide.
XX
XX Vaccines; accessory molecule; antigen; transport; presentation; allergy;
XX antibacterial; antiviral; antifungal; anti-allergic; antidiabetic;
XX anti-inflammation; anti-arthritic; anti-asthma; anticancer; treatment;
XX prevention; infection; bacterial; viral; fungal; autoimmune disease;
XX rheumatoid arthritis; diabetes; multiple sclerosis; pancreatitis;
XX inflammatory condition; psoriasis; immune deficiency; metastases;
XX cancer; Th1-type helper response; humoral; cellular response; B cell;
XX T cell; proliferation; immunoglobulin synthesis; isotype switching;
XX immunomodulator; immune response; asthma; human; HbsAg.
XX
XX Homo sapiens.
XX
XX MO9941368-A2.
XX
XX 19-AUG-1999.
XX
XX 10-FEB-1999; 99WC-US03020.
XX
XX 11-FEB-1998; 98US-0074294.
XX 11-FEB-1998; 98US-0021769.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Howard R, Punnonen J, Stemmer WPC, Whalen RG;
XX
XX WPI; 1999-508645/42.
XX
XX Identifying nucleic acid that directly or indirectly modulates the
XX immune response to a genetic vaccine vector, e.g. for prevention of
XX infection or cancer
XX
XX Example 3, Page 70; 105pp; English.
XX
XX This invention describes the identification of a novel polynucleotide (I)
XX that modulates the immune response to a genetic vaccine vector (A), or
XX encodes a polypeptide (II) with similar effect. The invention also
XX describes the identification of a polynucleotide (Ia) encoding an
XX accessory molecule (IIa) that improves transport and presentation of
XX antigen by a cell. The products of the invention have antibacterial,
XX antiviral, antifungal, anti-allergic, antidiabetic, anti-inflammatory,
XX anti-arthritic, anti-asthma, anticancer and immunomodulatory. Optimized
XX (I) are incorporated into (A), or (I) or its encoded (II) are
XX administered together with (A). (A) are used to treat or prevent
XX infections (bacterial, viral or fungal), autoimmune disease (e.g.
XX rheumatoid arthritis, diabetes or multiple sclerosis), other inflammatory
XX conditions (e.g. psoriasis or pancreatitis), immune deficiency, allergy,
XX asthma or cancer (including metastases). (I) are also used for
XX recombinant production of (II). (II) make it possible to tailor an immune
XX response to particular requirements, e.g. to direct a Th1-type helper
XX response to increase humoral or cellular responses (functioning as
XX adjuvant) to control B or T cell proliferation to induce immunoglobulin
XX synthesis or isotype switching. This sequence represents the HbsAg
XX (Pres2 plus S region) truncated peptide which is used in the method of
XX the invention.
XX
XX Sequence 102 AA;
XX
XX Query Match 100.0%; Score 61; DB 20; Length 102;
XX Best Local Similarity 100.0%; Pred. No. 0.00046;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 PLSISFRIGDP 12
XX |||||||||
XX 41 PLSISFRIGDP 52

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PN WO200020606-A1.
PD 13-APR-2000.
XX
XX 02-OCT-1998; 98WO-EP06298.
PF
PR 02-OCT-1998; 98WO-EP06298.
XX
XX 02-OCT-1998; 98WO-EP06298.
PA (REIM//) REIMANN H.
PA (SCH//) SCHIRMBECK R.
XX
XX Reimann H, SchirmbECK R;
XX
XX WPI; 2000-328936/28.
XX
PT Novel polynucleotide encoding a fusion protein which is stable in a
PT cell, useful for the production of peptides which coprecipitate
PT chaperones, by using truncated variants of the SV40 large T antigen
PT with an intact N-terminus -
XX
XX
XX Example 1; Page 26; 57pp; English.
XX
XX The present invention describes a polynucleotide (I) encoding a fusion
XX protein (P) (II) which is stable in a cell, and comprises a first
XX polypeptide (P1) and a second polypeptide (P2) which co-precipitates a
XX chaperone. The invention also provides methods for the production of
XX fusion proteins which comprise epitopes. Compositions comprising the
XX fusion proteins or epitopes of the invention are used as vaccines, and
XX for the production of antibodies. The methods provide an inexpensive
XX and efficient means of reliably expressing (poly)peptides comprising
XX epitopes. The present sequence represents the Hepatitis B virus (HBV)
XX preS protein sequence, which is used in an example from the present
XX invention.
XX
XX Sequence 164 AA;
XX
XX
XX Query Match 100.0%; Score 61; DB 21; Length 164;
XX Best Local Similarity 100.0%; Pred. No. 0.00077;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 PLSISFRIGDP 12
XX |||||
XX 150 PLSISFRIGDP 161
XX
XX
XX RESULT 10
XX AARI5617
XX ID AARI5617 standard; protein, 174 AA.
XX
XX AC AARI5617;
XX
XX XX
XX DT 25-MAR-2003 (updated)
XX DT 25-MAR-1992 (first entry)
XX
XX DE HBAAG pre-S region subtype ayw.
XX
XX T-cell epitope; vaccine; hepatitis B virus; antigen.
XX
XX Synthetic.
XX
XX OS WO9117768-A.
XX
XX PN 28-NOV-1991.
XX
XX PD 10-MAY-1991; 91WO-US03268.
XX
XX PF 11-MAY-1990; 90US-0522663.
XX
XX PR (SCRI-) SCRIPPS CLINIC & RE.
XX
XX PA
XX
XX PI Milich DR, Thornton GB;
XX
XX WPI; 1991-369007/50.

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XX Hepatitis B virus surface antigen epitope(s) - useful as vaccines,
PT immunogens or diagnostic reagents
XX
XX
PS Claim 1, Fig. 1, 91pp; English.
XX
CC The amino acid sequence is that of a pre-S T cell epitope polypeptide
CC of the pre-S (2) region of hepatitis B surface antigen Y (HBsAg/Y).
CC It can be used to prime or vaccinate a host to induce responsiveness
CC to HBV vaccine. The T cell epitope polypeptides can also be used as
CC immunogens that prime T cells that respond to native HBsAg B cell
CC epitope polypeptide. The T cell epitope polypeptides are also useful
CC as substitutes for carrier immunogens such as KLH and are safe,
CC defined and T cell-active. In addition to their use as vaccines, the
CC polypeptides can be used as immunogens for prodn. of antibodies. See
CC also AAR15618-R15622.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SQ Sequence 174 AA;
Query Match 100.0%; Score 61; DB 12; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLSISFRRIGDP 12
DB 160 PLSISFRRIGDP 171
RESULT 11
AAR23867 standard; protein; 174 AA.
XX
XX AAR23867;
AC 25-MAR-2003 (updated)
DT 11-NOV-1992 (first entry)
XX
XX Pre-S gene region translation product (1).
DE
XX
XX env gene; hepatitis B virus; HBV; S-protein; hydrophilic;
KM hepadnavirus; immune response; antibody; envelope.
XX
XX Hepatitis B virus, subtype ayw.
OS
XX
XX EP485361-A.
PN 13-MAY-1992.
XX
XX 25-APR-1987; 87BP-0100663.
PF
XX
XX 28-APR-1986; 86US-0856522.
PR
XX
XX (NYBL-) NY BLOOD CENT INC.
PA (CALY) CALIFORNIA INST OF TECHN.
XX
XX Kent SBH, Neurath AR;
PI
XX
XX WPI; 1992-161100/20.
DR
XX
XX Hepatitis B pre-S peptide immunogen and vaccine - for treatment
PT and diagnosis of hepatitis B
XX
XX
XX Disclosure; Fig 2; 59pp; English.
XX
XX The sequences given in AAR23867 - AAR23871 are amino acid sequences
CC deduced from sequences of the pre-S portion of the env genes
CC corresponding to several hepatitis B virus (HBV) subtypes. These
CC proteins have properties distinct from those of the S-protein in
CC that they have high hydrophilicity and a high percentage of charged
CC residues, an absence of Cys residues, the highest subtype-dependant
CC variability among HBV DNA gene products and little homology with
CC analogous sequences corresponding to nonhuman hepadnavirus. These

CC properties suggest that the pre-S gene coded portion of the HBV
CC envelope is expose to the surface of the virion, is a target for
CC the hosts immune response and is responsible for the host range of HBV
CC (limited to humans and some primates). Synthetic peptides and
CC antibodies against them, having predetermined specificity offer the
CC opportunity to explore the biological role of the pre-S protein moiety
CC of the HBV envelope. Portions of these amino acid sequences can be
CC used in a vaccine or in diagnostics for the detection of antigens and
CC antibodies, esp. those for the pre-S gene in sera of HBV infected
CC humans and certain animals, eg. chimpanzees.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SQ Sequence 174 AA;
Query Match 100.0%; Score 61; DB 13; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLSISFRRIGDP 12
DB 160 PLSISFRRIGDP 171
RESULT 12
AAB10597
ID AAB10597 standard; Protein; 215 AA.
XX
XX AAB10597;
AC 08-JAN-2001 (first entry)
DT
XX
XX HBV fusion protein comprising HBcAg and RGD.
DE
XX
XX Fusion protein; protein coat; virus-specific packaging signal; psi;
KM virus protein; cell permeability; cell-specific binding site; LMB;
KM large surface protein; core antigen; gene therapy.
XX
XX Hepatitis b virus.
OS
XX
XX Synthetic.
OS
XX
XX WO200046376-A2.
PN 10-AUG-2000.
XX
XX 04-FEB-2000; 2000WO-DE00363.
PF
XX
XX 05-FEB-1999; 99DE-1004800.
PR
XX
XX (HILD/) HILD E.
PA
XX
XX Hildt E, Hofschneider P;
PI
XX
XX WPI; 2000-514959/46.
DR N-PSDB; AAA71735.
DR
XX
XX Particle for cell-specific gene delivery, useful in gene therapy,
PT comprises nucleic acid in protein coat that includes a fusion protein
PT of viral protein, permeability peptide and cell-binding site
XX
XX
XX Claim 14; Fig 2; 34pp; German.
XX
XX This invention describes a novel particle (A), comprising a protein coat
CC with a fusion protein (FP), and, inside the coat, a nucleic acid (i)
CC including the sequence for a virus-specific packaging signal (psi) and a
CC structural gene. FP contains a virus protein (VP); a peptide (P) that
CC mediates cell permeability and a heterologous cell-specific binding site
CC (RGD). The invention also describes (1) producing (A) in which FP
CC contains an LHBs (large surface protein of hepatitis B virus (HBV)) and
CC RGD; (2) preparing (A) in which FP contains an HBV core antigen (HBcAg),
CC (P) and RGD; (3) FP; (4) DNA encoding FP; and (5) expression vector
CC containing the DNA of (d). The products of the invention are used in gene
CC therapy of cells and tissues, in vivo or ex vivo. This sequence
CC represents a fusion protein which is described in the method of the

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CC invention.
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 61; DB 21; Length 215;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PLSIFSRIGDP 12
DB 2 PLSIFSRIGDP 13

RESULT 13
AAR27471
ID AAR27471 standard; Protein; 281 AA.
XX
AC AAR27471;
XX
DT 25-MAR-2003 (updated)
DT 24-FEB-1993 (first entry)
XX
DE spsAg protein.
XX
KW Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
KW vaccinia virus; H6; early/late; promoter; NYVAC; recombinant; HBV L;
KW large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;
KW S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;
KW deletion loc1; recipient loc1.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..55
FT /label= S2
FT Region 56..281
FT /label= S
XX
PN MO9215672-A1.
XX
PD 17-SEP-1992.
XX
PF 09-MAR-1992; 92WO-US01906.
XX
PR 07-MAR-1991; 91US-0666056.
PR 11-JUN-1991; 91US-0713867.
PR 06-MAR-1992; 92US-0847951.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GP,
PI Limbach KU, Norton BK, Paciotti E, Perkins ME, Pincus SE;
PI Riviere M, Tartaglia J, Taylor J;
XX
DR WPI; 1992-331718/40.
DR N-PSDB; AAQ29103.
XX
PT Vaccine comprises recombinant, attenuated pox-virus - use for
PT vaccinating against viral infections such as rabies, hepatitis B,
PT HIV, HSV, EBV, CMV, mumps etc.
XX
PS Disclosure; Fig 9; 456pp; English.
XX
CC The sequence given is encoded by an expression cassette which
CC consists of the hepatitis B virus (HBV) M protein (small pre-S
CC antigen, spsAg) gene precisely linked to a modified synthetic
CC vaccinia virus H6 early/late promoter. This DNA sequence was used in
CC the construction of a NYVAC recombinant expressing the HBV gene.
CC Other HBV genes were also used in the construction. These were HBV
CC L (large pre-S antigen, lpsAg) and a fusion protein composed of the
CC entire pre-S region (S12/core, S1 + S2). Each of these gene sequences
CC were inserted individually into three different sites of NYVAC
CC separated by from each other by large regions of vaccinia DNA

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CC containing essential genes. NYVAC is a Copenhagen vaccine strain of
CC vaccinia virus which has been modified by deletion of six non-essential
CC regions of the genome encoding known or potential virulence factors.
CC The deletion loci were engineered as recipient loci for the insertion
CC of foreign genes. The spacing of the three inserted sequences ensured
CC that any recombination that did occur would lead to disruption of the
CC vaccinia genome and would cause unviable vaccinia virus. See also
CC AAQ35501-864.
CC (updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 61; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PLSIFSRIGDP 12
DB 41 PLSIFSRIGDP 52

RESULT 14
AAV32835
ID AAV32835 standard; Protein; 281 AA.
XX
AC AAV32835;
XX
DT 29-OCT-1999 (first entry)
XX
DE HBsAg PreS2-S region protein sequence.
XX
KW HBsAg; PreS2-S; recombinant antigen library; disease-related antigen;
KW multivalent antigenic polypeptide production; infection; allergen;
KW asthma; autoimmune disease; rheumatoid arthritis; diabetes; therapy;
KW multiple sclerosis; inflammatory condition; cancer; contraception;
KW immune response; hepatitis b surface antigen.
XX
OS Hepatitis b virus.
XX
PN WO9941383-A1.
XX
PD 19-AUG-1999.
XX
PF 10-FEB-1999; 99WO-US02944.
XX
PR 23-OCT-1998; 98US-0105509.
PR 11-FEB-1998; 98US-0021769.
PR 11-FEB-1998; 98US-0074294.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Bass SH, Howard R, Punnonen J, Stemmer WPC, Whalen RG;
XX
DR WPI; 1999-518452/43.
DR N-PSDB; AA210968.
XX
PT Recombinant multivalent antigenic polypeptide produced by
PT recombinant nucleic acid sequences and screening, used in vaccines
PT against e.g. infections and cancer
XX
PS Example 14; Fig 17; 153pp; English.
XX
CC This sequence is the hepatitis B virus (HBV) surface antigen (HBsAg)
CC PreS2-S region. This sequence was used to create a recombinant antigen
CC library. The library comprises recombinant nucleic acids encoding
CC antigenic polypeptides and is produced by recombination of at least two
CC forms of nucleic acid, differing by at least two nucleotides, encoding a
CC disease-related antigenic polypeptide. The library can be used to produce
CC a recombinant multivalent antigenic polypeptides of the invention, that
CC contains at least two antigenic determinants (AD) from different
CC polypeptides. The multivalent antigenic polypeptides are used in vaccines
CC to induce a protective or therapeutic response to a wide variety of
CC infectious agents (bacteria, viruses, parasites, including Plasmodium

```

CC falciparum); allergens; asthma; autoimmune disease (e.g. rheumatoid
 CC arthritis, diabetes, multiple sclerosis); other inflammatory conditions
 CC and cancer, also, where directed against sperm antigens, they can be used
 CC for contraception. The multivalent peptides can be evolved to induce an
 CC optimised immune response against a wide variety of antigens,
 CC particularly a broad spectrum response to many different strains of a
 CC pathogen, including strains that are likely to appear in the future.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 61; DB 20; Length 281;
 Best Local Similarity 100.0%; Pred. No. 0.0014;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
 |||||

Db 41 PLSIFSRIGDP 52

RESULT 15

ID AAR27472 standard; Protein; 389 AA.

AC AAR27472;

DT 25-MAR-2003 (updated)

DT 24-FEB-1993 (first entry)

XX 1psag protein.

XX Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;

KM vaccinia virus; hemorrhagic region; u promoter; NYVAC; recombinant;

KM HBV L; large pre-S antigen; 1psag; fusion protein; pre-S region;

XX S12/core; S1; S2; Copenhagen vaccine strain; vaccinia virus;

XX virulence factor; deletion loci; recipient loci.

OS Synthetic.

XX Key

XX region

XX misc_RNA

XX WO9215672-A1.

XX 17-SEP-1992.

XX 09-MAR-1992; 92WO-US01906.

XX 07-MAR-1991; 91US-0666056.

XX 11-JUN-1991; 91US-0713967.

XX 06-MAR-1992; 92US-0847951.

XX (VIRO-) VIROGENETICS CORP.

XX COX WI, De Taisne C, Francis J, Gettig RR, Johnson GP,

XX PI Limbach KJ, Norton EK, Paolletti E, Perkus ME, Pincus SE,

XX PI Riviere M, Tartaglia J, Taylor J;

XX WPI; 1992-331718/40.

XX N-PSDB; AAQ29104.

XX Vaccine comprises recombinant, attenuated pox-virus - use for

XX PT HIV, HSV, EBV, CMV, mumps etc.

XX Disclosure; Fig 11; 456pp; English.

XX The sequence given is encoded by an expression vector which comprises

CC the hepatitis B virus (HBV) L protein (large pre-S antigen, 1psag)

CC gene linked to the cowpox hemorrhagic region (u) promoter. This DNA
 CC sequence was used in the construction of a NYVAC recombinant
 CC expressing the HBV gene. Other HBV genes were also used in the
 CC construction. These were HBV M protein (small pre-S antigen, spsAg)
 CC and a fusion protein composed of the entire pre-S region (S12/core,
 CC S1 + S2). Each of these gene sequences were inserted individually
 CC into three different sites of NYVAC separated by from each other by
 CC large regions of vaccinia DNA containing essential genes. NYVAC is a
 CC Copenhagen vaccine strain of vaccinia virus which has been modified by
 CC deletion of six non-essential regions of the genome encoding known or
 CC potential virulence factors. The deletion loci were engineered as
 CC recipient loci for the insertion of foreign genes. The spacing of the
 CC three inserted sequences ensured that any recombination that did occur
 CC would lead to disruption of the vaccinia genome and would cause
 CC unviable vaccinia virus. See also AAQ35501-864.

XX SQ Sequence 389 AA;

Query Match 100.0%; Score 61; DB 13; Length 389;
 Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
 |||||

Db 149 PLSIFSRIGDP 160

RESULT 16

ID AAR27474 standard; Protein; 389 AA.

AC AAR27474;

DT 25-MAR-2003 (updated)

DT 24-FEB-1993 (first entry)

XX 13L promoter/S12/core gene.

XX Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;

KM vaccinia virus; Amsacta moorei entomopoxvirus; AMEPV; 42 KD; promoter;

KM NYVAC; recombinant; HBV L; large pre-S antigen; 1psag; fusion protein;

XX pre-S region; S12/core; S1; S2; Copenhagen vaccine strain;

XX vaccinia virus; virulence factor; deletion loci; recipient loci.

OS Synthetic.

XX Key

XX region

XX Region

XX WO9215672-A1.

XX 17-SEP-1992.

XX 09-MAR-1992; 92WO-US01906.

XX 07-MAR-1991; 91US-0666056.

XX 11-JUN-1991; 91US-0713967.

XX 06-MAR-1992; 92US-0847951.

XX (VIRO-) VIROGENETICS CORP.

XX COX WI, De Taisne C, Francis J, Gettig RR, Johnson GP,

XX PI Limbach KJ, Norton EK, Paolletti E, Perkus ME, Pincus SE,

XX PI Riviere M, Tartaglia J, Taylor J;

XX WPI; 1992-331718/40.

XX N-PSDB; AAQ29106.

XX Vaccine comprises recombinant, attenuated pox-virus - use for

XX PT HIV, HSV, EBV, CMV, mumps etc.

XX Disclosure; Fig 11; 456pp; English.

XX The sequence given is encoded by an expression vector which comprises

CC the hepatitis B virus (HBV) L protein (large pre-S antigen, 1psag)

CC repeats has been deleted and the protein comprising the C-terminal
 CC cysteine of HBcAg. The deleted region may be replaced by an epitope
 CC from a protein other than HBcAg, in which case the HBcAg acts as a
 CC carrier to present the epitope to the immune system. This chimeric
 CC protein or its nucleic acid is useful as a vaccine or in a method of
 CC prophylactic or therapeutic vaccination of the human or animal body,
 CC particularly against HBV. The nucleic acid encoding the protein may
 CC be used in gene therapy or DNA vaccination protocols. The chimeric
 CC protein or its nucleic acid may also be used as the basis of a
 CC prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis
 CC A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth
 CC disease, polio, herpes, rabies, acquired immunodeficiency syndrome
 CC (AIDS), dengue fever, yellow fever, malaria, tuberculosis, whooping
 CC cough, salmonellosis, typhoid, food poisoning, diarrhoea, meningitis
 CC or gonorrhoea. The present sequence is a C-terminally truncated chimeric
 CC derivative of Hepatitis B virus core antigen (HBc) into which HBV
 CC pre-S2 peptide is inserted.

SQ Sequence 67 AA;

Query Match 96.7%; Score 59; DB 23; Length 67;
 Best Local Similarity 91.7%; Pred. No. 0.00072;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
 DB 48 PLSSTFSRIGDP 59

RESULT 23

ID AAR15618 standard; protein; 174 AA.

AC AAR15618;

DT 25-MAR-2003 (updated)

DT 25-MAR-1992 (first entry)

DE HBsAg pre-S region subtype adyw.

KM T-cell epitope; vaccine; hepatitis B virus; antigen.

OS Synthetic.

PN WO9117768-A.

PD 26-NOV-1991.

PF 10-MAY-1991; 91WO-US03268.

PR 11-MAY-1990; 90US-0522663.

PA (SCR1-) SCRIPPS CLINIC & RE.

PI Milich DR, Thornton GB;

DR WPI; 1991-369007/50.

PT Hepatitis B virus surface antigen epitope(s) - useful as vaccines,
 immunogens or diagnostic reagents

PS Claim 2; Fig 1; 91np; English.

XX The amino acid sequence is that of a pre-S T cell epitope polypeptide
 CC composite of the pre-S (2) regions of hepatitis B surface antigens Y
 CC (HBsAg/Y) and d (HBsAg/d). It can be used to prime or vaccinate a host
 CC to induce responsiveness to HBV vaccine. The T cell epitope poly-
 CC peptides can also be used as immunogens that prime T cells that respond
 CC to native HBsAg B cell epitope polypeptide. The T cell epitope poly-
 CC peptides are also useful as substitutes for carrier immunogens such as
 CC KLH and are safe, defined and T cell-active. In addition to their use
 CC as vaccines, the polypeptides can be used as immunogens for prodn. of
 CC antibodies. See also AAR15617-R15622.

CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 174 AA;

QY 1 PLSSTFSRIGDP 12
 DB 160 PLSSTFSRIGDP 171

Query Match 96.7%; Score 59; DB 12; Length 174;
 Best Local Similarity 91.7%; Pred. No. 0.002;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 24

ID AAR23868 standard; Protein; 174 AA.

AC AAR23868;

DT 25-MAR-2003 (updated)

DT 11-NOV-1992 (first entry)

DE Pre-S gene region translation product (2).

KM env gene; hepatitis B virus; HBV; S-protein; hydrophilic;
 KM hepadnavirus; immune response; antibody; envelope.

OS Hepatitis B virus, subtype adyw.

PN EP485361-A.

PD 13-MAY-1992.

PF 25-APR-1987; 87EP-0100663.

PR 28-APR-1986; 86US-0856522.

PA (NYBL-) NY BLOOD CENT INC.

PA (CALV) CALIFORNIA INST OF TECHN.

PI Kent SBH, Neurath AR;

DR WPI; 1992-161100/20.

PT Hepatitis B pre-S peptide immunogen and vaccine - for treatment
 and diagnosis of hepatitis B

PS Disclosure; Fig 2; 59np; English.

XX The sequences given in AAR23867 - AAR23871 are amino acid sequences
 CC deduced from sequences of the pre-S portion of the env genes
 CC corresponding to several hepatitis B virus (HBV) subtypes. These
 CC proteins have properties distinct from those of the S-protein in
 CC that they have high hydrophilicity and a high percentage of charged
 CC residues, an absence of Cys residues, the highest subtype-dependent
 CC variability among HBV DNA gene products and little homology with
 CC analogous sequences corresponding to nonhuman hepadnavirus. These
 CC properties suggest that the pre-S gene coded portion of the HBV
 CC envelope is exposed to the surface of the virion, is a target for
 CC (limited to humans and some primates). Synthetic peptides and
 CC antibodies against them, having predetermined specificity offer the
 CC opportunity to explore the biological role of the pre-S protein moiety
 CC of the HBV envelope. Portions of these amino acid sequences can be
 CC used in a vaccine or in diagnostics for the detection of antigens and
 CC antibodies, esp. those for the pre-S gene in sera of HBV infected
 CC humans and certain animals, eg. chimpanzees.
 CC (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 174 AA;

Query Match 96.7%; Score 59; DB 13; Length 174;
 Best Local Similarity 91.7%; Pred. No. 0.002;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PLSIFSRIGDP 12
 ||:|||||||
 Db 160 PLSIFSRIGDP 171

RESULT 25
 AAB58074
 ID AAB58074 standard; Protein; 174 AA.
 XX
 AC AAB58074;
 XX
 DT 07-MAR-2003 (first entry)
 XX

DE Hepatitis B virus subtype ayw recombinant pre-S protein.
 XX
 KW HBV, pre-S protein; adjuvant; vaccine; mutant; mutein.
 XX
 OS Hepatitis B virus.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 15
 FT /note= "wild-type Asn substituted by His"
 FT Misc-difference 123
 FT /note= "wild-type Asn substituted by His"

XX WO200294866-A1.
 XX
 XX 28-NOV-2002.
 XX

XX 02-MAY-2002; 2002MO-KR00820.
 XX
 XX 25-MAY-2001; 2001KR-0029002.
 XX

XX (DOBE-) DOBEEL CORP.
 XX

XX Mun H, Kim K, Yum J, Ahn B, Yi S, Seemun Y, Park J;
 XX

XX WPI, 2003-120785/11.
 XX

XX Modified pre-S of hepatitis B virus (HBV) enhancing immunogenicity of a
 PT general vaccine antigen, useful for the diagnosis of, prophylactic
 PT and/or therapeutic treatment of HBV infection -

XX Disclosure; Page 60-61; 68pp; English.
 XX

XX The present sequence is the protein sequence of a recombinant pre-S
 CC protein of hepatitis B virus (HBV) subtype ayw, produced by
 CC Saccharomyces cerevisiae 2805/PII20-pre-S (adr). Cultivation of
 CC this transformant at 30 degrees C for 24-48 hours in a fed-batch
 CC system yielded recombinant pre-S, which was secreted at a level of
 CC 850 mg/l culture medium. The recombinant pre-S was purified by
 CC removing yeast cells from the broth, concentrating the cell-free
 CC broth, dialysing using an ultra-fine membrane, and separating using
 CC ion exchange and molecular size separation columns. The
 CC recombinant pre-S is modified from the native form by substitution
 CC of Asn glycosylation sites at positions 15 and 123 by histidine
 CC residues. The recombinant pre-S protein can be used as a component
 CC of an HBV vaccine for generating immunity for HBV, as an adjuvant,
 CC and in diagnostic compositions. The modifications improve the
 CC immunogenicity of the HBV S antigen, providing an improved
 CC prophylactic vaccine and a therapeutic vaccine for the treatment of
 CC chronic HBV carriers.
 XX

XX Sequence 174 AA;
 SQ

Query Match 96.7%; Score 59; DB 24; Length 174;
 Best Local Similarity 91.7%; Pred. No. 0.002;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12

Db 160 PLSIFSRIGDP 171
 ||:|||||||

RESULT 26
 AAB10596
 ID AAB10596 standard; Protein; 347 AA.
 XX
 AC AAB10596;
 XX
 DT 08-JAN-2001 (first entry)
 XX

DE HBV fusion protein comprising LHB and RGD.
 XX
 KW Fusion protein; protein coat; virus-specific packaging signal; psi;
 XX virus protein; cell permeability; cell-specific binding site; LHB;
 XX large surface protein; core antigen; gene therapy.
 XX

XX Hepatitis b virus.
 XX
 OS Synthetic.
 XX

XX WO200046376-A2.
 XX

XX 10-AUG-2000.
 XX

XX 04-FEB-2000; 2000MO-DE00363.
 XX

XX 05-FEB-1999; 99DE-1004800.
 XX

XX (HILD/) HILDT E.
 XX

XX Hildt E, Hofschneider P;
 XX

XX WPI, 2000-514959/46.
 XX

XX N-PSDB; AAA71734.
 XX

XX Particle for cell-specific gene delivery, useful in gene therapy,
 PT comprises nucleic acid in protein coat that includes a fusion protein
 PT of viral protein, permeability peptide and cell-binding site -

XX Claim 14; Fig 1; 34pp; German.
 XX

XX This invention describes a novel particle (A), comprising a protein coat
 CC with a fusion protein (FP), and, inside the coat, a nucleic acid (i)
 CC including the sequence for a virus-specific packaging signal (psi) and a
 CC structural gene. FP contains a virus protein (VP); a peptide (P) that
 CC mediates cell permeability and a heterologous cell-specific binding site
 CC (RGD). The invention also describes (1) producing (A) in which FP
 CC contains an LHBs (large surface protein of hepatitis B virus (HBV)) and
 CC RGD; (2) preparing (A) in which FP contains an HBV core antigen (HBcAg),
 CC (P) and RGD; (3) FP; (4) DNA encoding FP; and (5) expression vector
 CC containing the DNA of (d). The products of the invention are used in gene
 CC therapy of cells and tissues, in vivo or ex vivo. This sequence
 CC represents a fusion protein which is described in the method of the
 CC invention.
 XX

XX Sequence 347 AA;
 SQ

Query Match 96.7%; Score 59; DB 21; Length 347;
 Best Local Similarity 91.7%; Pred. No. 0.0043;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
 ||:|||||||

Db 107 PLSIFSRIGDP 118

RESULT 27

AAG66931
 ID AAG66931 standard; Protein; 389 AA.
 XX

XX AAG66931;
 XX

DT 19-OCT-2001 (first entry)
 XX HBV genotype D pres1/pres2/HBsAg polypeptide.
 DE
 XX Hepatitis B virus; HBV; preCore; Core; pres1; pres2; HBS; HBx; HBpPol;
 KW HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBsAg.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200140279-A2.
 PD 07-JUN-2001.
 XX
 PF 20-NOV-2000; 2000WO-EP11526.
 XX
 PR 03-DEC-1999; 99EP-0870252.
 PR 07-DEC-1999; 99US-0169287.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Stuyver L, Van Geyt C, De Gendt S;
 XX
 DR WPI; 2001-374785/39.
 XX
 PT Novel isolated and/or purified hepatitis B virus polypeptide and
 PT polynucleotide sequences that are phylogenetically different from HBV
 PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
 PT therapy -
 XX
 PS Example 3; Fig 6; 94pp; English.
 XX
 CC The invention relates to the complete nucleic acid sequence of a new
 CC human hepatitis B virus (HBV) genotype, provisionally named genotype
 CC G. This genotype was found with a high prevalence in patients
 CC chronically infected with HBV and residing in Europe and the USA. The
 CC invention relates to a fully defined sequence of 3248 nucleotides as
 CC given in specification, a sequence with 92% identity to the given
 CC sequence, or sequence that is degenerate to the mentioned sequences.
 CC These polynucleotides are useful for HBV genotyping. The proteins
 CC encoded by the polynucleotides are useful for detecting antibodies in
 CC a biological sample. Ligands that bind to the proteins and antibodies
 CC directed against the proteins are useful for detecting the proteins
 CC and for detecting HBcAg and HBsAg (precore precursor proteins). They
 CC are also useful for preparing a vaccine or medicament for treating
 CC HBV infections. The present sequence is provided in an amino acid
 CC sequence alignment of the pres1, pres2 and HBsAg open reading frame
 CC of the different HBV genotypes.
 CC
 SQ Sequence 389 AA;
 XX
 QY Query Match 96.7%; Score 59; DB 22; Length 389;
 Best Local Similarity 91.7%; Pred. No. 0.0048;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 149 PLSISFRRIGDP 12
 149 PLSISFRRIGDP 160
 XX
 RESULT 28
 ABP55073
 ID ABP55073 standard; Protein; 389 AA.
 XX
 AC ABP55073;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE Hepatitis B virus mutant envelope protein.
 XX
 KW HBV; HBsAg; surface antigen; envelope; diagnosis; vaccine; mutant;
 KW muten.
 XX
 OS Hepatitis B virus.
 XX

XX Key Location/Qualifiers
 FH Peptide 1..108
 FT /label= Pres1
 FT Peptide 109..163
 FT /label= Pres2
 FT Protein 164..389
 FT /label= Small_envelope
 XX
 PN WO200279217-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US09227.
 XX
 PR 30-MAR-2001; 2001US-0821877.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Coleman PF, Mushahwar IA;
 XX
 DR WPI; 2003-040642/03.
 DR N-PSDB; ABV75781.
 XX
 PT New nucleotide sequences, useful for detecting compounds that bind to
 PT gp41 protein or antibodies to the Hepatitis B virus surface antigen
 PT mutant or for creating primers and probes -
 XX
 PS Claim 2; Fig 2; 43pp; English.
 XX
 CC The present sequence is the protein sequence of the entire
 CC envelope protein of a mutant hepatitis B virus (HBV) strain
 CC isolated from a French sample identified as 990525169. This is an
 CC HBV subtype ayw2, genotype D strain which contains mutations leading
 CC to 3 amino acid substitutions compared to the wild-type: Thr to Ala
 CC 123, which affects the H166 epitope; Tyr to Leu 199, which is
 CC outside the 'a' determinant; and Ser to Thr 207, which is also
 CC outside the 'a' determinant. The present invention relates to the
 CC novel HBV mutant which has a modified 'a' determinant as a result
 CC of T123 amino acid substitution, and to methods of detecting this
 CC mutant, and/or antibodies to the mutant, in patient samples. The
 CC identification and detection of mutant HBV may lead to improved
 CC vaccine development and detection systems.
 CC
 SQ Sequence 389 AA;
 XX
 QY Query Match 96.7%; Score 59; DB 24; Length 389;
 Best Local Similarity 91.7%; Pred. No. 0.0048;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 149 PLSISFRRIGDP 12
 149 PLSISFRRIGDP 160
 XX
 RESULT 29
 AAR12394
 ID AAR12394 standard; Protein; 174 AA.
 XX
 AC AAR12394;
 XX
 DT 29-AUG-1991 (first entry)
 XX
 DE Pre-S antigen.
 XX
 KW HBV; pre-SAg.
 XX
 OS Hepatitis B virus.
 XX
 PN JP03108494-A.
 XX
 PD 08-MAY-1991.
 XX

PF 19-SEP-1989; 89JP-0242722.
XX
PR 19-SEP-1989; 89JP-0242722.
XX
PA (MITU) MITSUBISHI KASEI CORP.
XX
XX WPI; 1991-180929/25.
DR N-PSDB; AAQ11985.
XX
XX Efficient prepn. of hepatitis B virus pre-S-antigen - comprises
PT introducing of signal peptide DNA fragment and antigen coding DNA
PT fragment to expression vector promoter.
XX
XX Disclosure; Fig 1; 16pp; Japanese.
XX
CC The protein is expressed by a vector contg. the code for the antigen.
CC It can be used as a vaccine for HBV. Antibodies can also be prepd.
CC against pre-SAg and used for diagnosis of HBV.
XX
SQ Sequence 174 AA;

Query Match 88.5%; Score 54; DB 12; Length 174;
Best Local Similarity 83.3%; Pred. No. 0.019;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
|:|||||
Db 160 PISIFSRIGDP 171

RESULT 30
AAR15622
ID AAR15622 standard; protein; 174 AA.
XX
AC AAR15622;
XX
DT 25-MAR-2003 (updated)
DT 25-MAR-1992 (first entry)
XX
DE HBsAg pre-S region subtype adr.
XX
KM T-cell epitope; vaccine; hepatitis B virus; antigen.
XX
OS Synthetic.
XX
PN WO9117768-A.
XX
PD 28-NOV-1991.
XX
PF 10-MAY-1991; 91WO-US03268.
XX
PR 11-MAY-1990; 90US-0522663.
XX
PA (SCRI-) SCRIPPS CLINIC & RE.
XX
XX Milich DR, Thornton GB;
PI WPI; 1991-369007/50.
DR
XX Hepatitis B virus surface antigen epitope(s) - useful as vaccines,
PT immunogens or diagnostic reagents
XX
XX Claim 1; Fig 1; 91pp; English.
XX
CC The amino acid sequence is that of a pre-S T cell epitope polypeptide
CC of the pre-S (2) region of hepatitis B surface antigen d (HBsAg/d).
CC It can be used to prime or vaccinate a host to induce responsiveness
CC to HBV vaccine. The T cell epitope polypeptides can also be used as
CC immunogens that prime T cells that respond to native HBsAg B cell
CC epitope polypeptide. The T cell epitope polypeptides are also useful
CC as substitutes for carrier immunogens such as KdH and are safe,
CC defined and T cell-active. In addition to their use as vaccines, the
CC polypeptides can be used as immunogens for prodn. of antibodies. See

CC also AAR15617-R15621.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 174 AA;

Query Match 88.5%; Score 54; DB 12; Length 174;
Best Local Similarity 83.3%; Pred. No. 0.019;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
|:|||||
Db 160 PISIFSRIGDP 171

RESULT 31
AAR23871
ID AAR23871 standard; Protein; 174 AA.
XX
AC AAR23871;
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1992 (first entry)
XX
DE Pre-S gene region translation product (5).
XX
XX env gene; hepatitis B virus; HBV; S-protein; hydrophilic;
KM hepadnavirus; immune response; antibody; envelope.
XX
OS Hepatitis B virus, subtype adr.
XX
PN EP485361-A.
XX
PD 13-MAY-1992.
XX
PF 25-APR-1987; 87EP-0100663.
XX
PR 28-APR-1986; 86US-0856522.
XX
PA (NYBL-) NY BLOOD CENT INC.
PA (CALY) CALIFORNIA INST OF TECHN.
XX
PI Kent SBH, Neurath AR;
XX
DR WPI; 1992-161100/20.
XX
PT Hepatitis B pre-S peptide immunogen and vaccine - for treatment
PT and diagnosis of hepatitis B
XX
PS Disclosure; Fig 2; 59pp; English.
XX
CC The sequences given in AAR23867 - AAR23871 are amino acid sequences
CC deduced from sequences of the pre-S portion of the env genes
CC corresponding to several hepatitis B virus (HBV) subtypes. These
CC proteins have properties distinct from those of the S-protein in
CC that they have high hydrophilicity and a high percentage of charged
CC residues, an absence of Cys residues, the highest subtype-dependant
CC variability among HBV DNA gene products and little homology with
CC analogous sequences corresponding to nonhuman hepadnavirus. These
CC properties suggest that the pre-S gene coded portion of the HBV
CC envelope is expose to the surface of the virion, is a target for
CC the hosts immune response and is responsible for the host range of HBV
CC (limited to humans and some primates). Synthetic peptides and
CC antibodies against them, having predetermined specificity offer the
CC opportunity to explore the biological role of the pre-S protein moiety
CC of the HBV envelope. Portions of these amino acid sequences can be
CC used in a vaccine or in diagnostics for the detection of antigens and
CC antibodies, esp. those for the pre-S gene in sera of HBV infected
CC humans and certain animals, eg. chimpanzees.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 174 AA;

Query Match 88.5%; Score 54; DB 13; Length 174;

Best Local Similarity 83.3%; Pred. No. 0.019;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFRRIGDP 12
|:|||||
Db 160 PLSISFRRIGDP 171

RESULT 32
ABP58070
ID ABP58070 standard; Protein; 174 AA.

AC ABP58070;

DT 07-MAR-2003 (first entry)

DE Hepatitis B virus modified pre-S polypeptide pre-S-15m.

KW HBV, pre-S protein; adjuvant; vaccine; mutant; mutein.

OS Hepatitis B virus.

XX Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 15 /note="wild-type Asn substituted by His"

PN WO200294866-A1.

XX 28-NOV-2002.

PF 02-MAY-2002; 2002WO-KR00820.

PR 25-MAY-2001; 2001KR-0029002.

XX (DOBE-) DOBEEL CORP.

PI Mun H, Kim K, Yum J, Ahn B, Yi S, Seemun Y, Park J;

DR WPI; 2003-120785/11.

PT Modified pre-S of hepatitis B virus (HBV) enhancing immunogenicity of a

XX general vaccine antigen, useful for the diagnosis of, prophylactic

XX and/or therapeutic treatment of HBV infection -

XX Claim 4; Page 62-63; 68pp; English.

CC The present sequence is the protein sequence of a modified pre-S
CC protein, pre-S-15m, of hepatitis B virus (HBV) in which the native
CC asparagine residue at position 15 is substituted by a histidine
CC residue. This removes one of the two glycosylation sites (the
CC other is Asn-123) from the protein. The pre-S-15m protein is
CC produced using a yeast (especially *Saccharomyces cerevisiae*)
CC recombinant expression system. It can be used as a component of an
CC HBV vaccine for generating immunity for HBV, and as an adjuvant.
CC The modification improves the immunogenicity of the HBV S antigen,
CC providing an improved prophylactic vaccine and a therapeutic
CC vaccine for the treatment of chronic HBV carriers.

XX Sequence 174 AA;

Query Match 88.5%; Score 54; DB 24; Length 174;

Best Local Similarity 83.3%; Pred. No. 0.019;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFRRIGDP 12
|:|||||
Db 160 PLSISFRRIGDP 171

RESULT 33

ABP58071
ID ABP58071 standard; Protein; 174 AA.

XX ABP58071;

DT 07-MAR-2003 (first entry)

DE Hepatitis B virus modified pre-S polypeptide pre-S-123m.

KW HBV, pre-S protein; adjuvant; vaccine; mutant; mutein.

OS Hepatitis B virus.

XX Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 123 /note="wild-type Asn substituted by His"

PN WO200294866-A1.

XX 28-NOV-2002.

PF 02-MAY-2002; 2002WO-KR00820.

PR 25-MAY-2001; 2001KR-0029002.

XX (DOBE-) DOBEEL CORP.

PI Mun H, Kim K, Yum J, Ahn B, Yi S, Seemun Y, Park J;

DR WPI; 2003-120785/11.

PT Modified pre-S of hepatitis B virus (HBV) enhancing immunogenicity of a
PT general vaccine antigen, useful for the diagnosis of, prophylactic
PT and/or therapeutic treatment of HBV infection -

XX Claim 4; Page 63-64; 68pp; English.

CC The present sequence is the protein sequence of a modified pre-S
CC protein, pre-S-123m, of hepatitis B virus (HBV) in which the native
CC asparagine residue at position 123 is substituted by a histidine
CC residue. This removes one of the two glycosylation sites (the
CC other is Asn-15) from the protein. The pre-S-123m protein is
CC produced using a yeast (especially *Saccharomyces cerevisiae*)
CC recombinant expression system. It can be used as a component of an
CC HBV vaccine for generating immunity for HBV, and as an adjuvant.
CC The modification improves the immunogenicity of the HBV S antigen,
CC providing an improved prophylactic vaccine and a therapeutic
CC vaccine for the treatment of chronic HBV carriers.

XX Sequence 174 AA;

Query Match 88.5%; Score 54; DB 24; Length 174;

Best Local Similarity 83.3%; Pred. No. 0.019;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFRRIGDP 12
|:|||||
Db 160 PLSISFRRIGDP 171

RESULT 34

ABP58072
ID ABP58072 standard; Protein; 174 AA.

AC ABP58072;

DT 07-MAR-2003 (first entry)

DE Hepatitis B virus modified pre-S polypeptide pre-S-dm.

KW HBV, pre-S protein; adjuvant; vaccine; mutant; mutein.

XX Hepatitis B virus.

OS Synthetic.

```

XX Key Location/Qualifiers
FH Misc-difference 15
FT /note= "wild-type Asn substituted by His"
FT Misc-difference 123
FT /note= "wild-type Asn substituted by His"
XX
XX WO200294866-A1.
XX
XX PD 28-NOV-2002.
XX
XX PF 02-MAY-2002; 2002WO-KR00820.
XX
XX PR 25-MAY-2001; 2001KR-0029002.
XX
XX PA (DOBE-) DOBEEL CORP.
XX
XX PI Mun H, Kim K, Yum J, Ahn B, Yi S, Seomun Y, Park J;
XX WPI, 2003-120785/11.
XX
XX DR WPI, 2003-120785/11.
XX
XX PT Modified pre-S of hepatitis B virus (HBV) enhancing immunogenicity of a
XX general vaccine antigen, useful for the diagnosis of, prophylactic
XX and/or therapeutic treatment of HBV infection -
XX
XX PS Claim 4; Page 64-65; 68pp; English.
XX
XX CC The present sequence is the protein sequence of a modified pre-S
XX protein, pre-S-dm, of hepatitis B virus (HBV) in which the native
XX asparagine residues at positions 15 and 123 are each substituted by
XX histidine residues, thereby removing both glycosylation sites of
XX the protein. The pre-S-dm protein is produced using a yeast
XX (especially Saccharomyces cerevisiae) recombinant expression system.
XX It can be used as a component of an HBV vaccine for generating
XX immunity for HBV, and as an adjuvant. The modification improves
XX the immunogenicity of the HBV S antigen, providing an improved
XX prophylactic vaccine and a therapeutic vaccine for the treatment of
XX chronic HBV carriers.
XX
XX SQ Sequence 174 AA;
XX
XX Query Match 88.5%; Score 54; DB 24; Length 174;
XX Best Local Similarity 83.3%; Pred. No. 0.019;
XX Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 PLSISFSRIGDP 12
XX |:|||||
XX Db 160 PLSISFSRIGDP 171
XX
XX RESULT 35
XX ID AAP58073 standard; Protein; 174 AA.
XX
XX AC AAP58073;
XX
XX DT 07-MAR-2003 (first entry)
XX
XX DE Hepatitis B virus subtype adr recombinant pre-S protein.
XX
XX KW HBV; pre-S protein; adjuvant; vaccine; mutant; mutein.
XX
XX OS Hepatitis B virus.
XX
XX PA Synthetic.
XX
XX Key Location/Qualifiers
XX FH Misc-difference 15
XX /note= "wild-type Asn substituted by His"
XX FT Misc-difference 123
XX /note= "wild-type Asn substituted by His"
XX
XX WO200294866-A1.
XX

```

```

PD 28-NOV-2002.
XX
XX PF 02-MAY-2002; 2002WO-KR00820.
XX
XX PR 25-MAY-2001; 2001KR-0029002.
XX
XX PA (DOBE-) DOBEEL CORP.
XX
XX PI Mun H, Kim K, Yum J, Ahn B, Yi S, Seomun Y, Park J;
XX WPI, 2003-120785/11.
XX
XX DR WPI, 2003-120785/11.
XX
XX PT Modified pre-S of hepatitis B virus (HBV) enhancing immunogenicity of a
XX general vaccine antigen, useful for the diagnosis of, prophylactic
XX and/or therapeutic treatment of HBV infection -
XX
XX PS Disclosure; Page 59-60; 68pp; English.
XX
XX CC The present sequence is the protein sequence of a recombinant pre-S
XX protein of hepatitis B virus (HBV) subtype adr, produced by
XX Saccharomyces cerevisiae 2805/pIL20-pre-S (adr). Cultivation of
XX this transformant at 30 degrees C for 24-48 hours in a fed-batch
XX system yielded recombinant pre-S, which was secreted at a level of
XX 850 mg/l culture medium. The recombinant pre-S was purified by
XX removing yeast cells from the broth, concentrating the cell-free
XX broth, dialysing using an ultra-fine membrane, and separating using
XX ion exchange and molecular size separation columns. The
XX recombinant pre-S is modified from the native form by substitution
XX of Asn glycosylation sites at positions 15 and 123 by histidine
XX residues. The recombinant pre-S protein can be used as a component
XX of an HBV vaccine for generating immunity for HBV, as an adjuvant,
XX and in diagnostic compositions. The modifications improve the
XX immunogenicity of the HBV S antigen, providing an improved
XX prophylactic vaccine and a therapeutic vaccine for the treatment of
XX chronic HBV carriers.
XX
XX SQ Sequence 174 AA;
XX
XX Query Match 88.5%; Score 54; DB 24; Length 174;
XX Best Local Similarity 83.3%; Pred. No. 0.019;
XX Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 PLSISFSRIGDP 12
XX |:|||||
XX Db 160 PLSISFSRIGDP 171
XX
XX RESULT 36
XX ID AAP60163 standard; Protein; 281 AA.
XX
XX AC AAP60163;
XX
XX DT 25-MAR-2003 (updated)
XX DT 02-JUL-1991 (first entry)
XX
XX DE Subtype adr hepatitis B virus surface antigen P31.
XX
XX KW Hepatitis B virus; subtype adr; surface antigen P31; vaccine;
XX
XX OS Hepatitis B virus.
XX
XX PA EPI71908-A.
XX
XX PN 19-FEB-1986.
XX
XX PD 03-JUL-1985; 85RP-0304735.
XX
XX PF 03-JUN-1985; 85WO-JP00306.
XX PR 11-JUL-1984; 84WO-JP00356.
XX PR 04-SEP-1984; 84WO-JP00423.
XX PR 12-DEC-1984; 84WO-JP00585.
XX

```

PA (TAKE) TAKEDA CHEM IND LTD.
 PA (KIKU/) KIKUCHI M.
 XX
 PI Kikuchi M, Fujisawa Y, Ikeyama S, Nishimura O;
 XX
 DR WPI, 1986-049762/08.
 DR N-PSDB; AAN60129.
 XX
 PT New non-glycosylated hepatitis-B virus surface antigen p31
 PT protein - is prepd. by recombinant DNA methods for use in
 PT vaccines for diagnosis, preventing and treating hepatitis-B virus
 PT infections
 XX
 PS Disclosure; Fig. 1; 85bp; English.
 XX
 CC Subtype adr hepatitis B virus surface antigen p31 has the same biological
 CC activity as known hepatitis B virus surface antigen small particles obtd.
 CC from the blood of hepatitis B virus-infected individuals. The antigen is
 CC useful in vaccines for the diagnosis, prevention and/or treatment of
 CC hepatitis B infections in the same way as the small particles.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX
 SQ Sequence 281 AA;
 Query Match 88.5%; Score 54; DB 7; Length 281;
 Best Local Similarity 83.3%; Pred. No. 0.032;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLSSIFSRIGDP 12
 |:|||||
 Db 41 PISSIFSRIGDP 52
 RESULT 37
 AAP60560
 ID AAP60560 standard; Protein; 281 AA.
 XX
 AC AAP60560;
 XX
 DT 25-MAR-2003 (updated)
 DT 04-JUL-1991 (first entry)
 XX
 DE Hepatitis B virus p31 antigen subtype adr.
 XX
 KW Vaccine; hepatitis.
 XX
 OS Hepatitis B virus.
 XX
 PN WO8600640-A.
 PN
 PD 30-JAN-1986.
 PD
 PF 11-JUL-1984; 84WO-JP00356.
 PF
 PR 11-JUL-1984; 84WO-JP00356.
 PR
 PR 03-JUN-1985; 85WO-JP00306.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 PI Kikuchi M, Fujisawa Y;
 PI
 XX WPI; 1986-042123/06.
 DR
 DR N-PSDB; AAN60461.
 DR
 PT Hepatitis B virus surface antigen p31 from culture of
 PT transformant - containing p31 dna at 3'-terminal promoter region.
 PT
 PS Disclosure; Fig 1; 43bp; Japanese.
 PS
 CC The p31 antigen may be isolated from a transformed host in high
 CC yields, it may be used as a vaccine against infection by the
 CC hepatitis B virus.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC

XX
 SQ Sequence 281 AA;
 Query Match 88.5%; Score 54; DB 7; Length 281;
 Best Local Similarity 83.3%; Pred. No. 0.032;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLSSIFSRIGDP 12
 |:|||||
 Db 41 PISSIFSRIGDP 52
 RESULT 38
 AAP60617
 ID AAP60617 standard; Protein; 281 AA.
 XX
 AC AAP60617;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-OCT-1991 (first entry)
 XX
 DE C-terminal defective hepatitis B surface antigen.
 XX
 KW Vaccine; HBsAg.
 XX
 OS Hepatitis B virus.
 XX
 PN WO8605808-A.
 PN
 PD 09-OCT-1986.
 PD
 PF 03-APR-1985; 85WO-JP00161.
 PF
 PR 03-APR-1985; 85WO-JP00161.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 PI WPI; 1986-278821/42.
 DR
 DR N-PSDB; AAN60613.
 DR
 XX C-terminal defective hepatitis B virus surface antigen - obtd. by
 PT culture of transformant contg. recombinant DNA coding for
 PT defective antigen with promoter upstream and stop codon
 PT downstream.
 XX
 PS Disclosure; Fig 7; 41bp; Japanese.
 XX
 CC The gene product is a C-terminal defective Hepatitis B surface
 CC antigen. The product may be incorporated into a vaccine, or Mabs
 CC raised to it used in diagnosis of the viral infection.
 CC The gene may be expressed in a transformed E.coli host, under the
 CC control of a trp promoter.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX
 SQ Sequence 281 AA;
 Query Match 88.5%; Score 54; DB 7; Length 281;
 Best Local Similarity 83.3%; Pred. No. 0.032;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLSSIFSRIGDP 12
 |:|||||
 Db 41 PISSIFSRIGDP 52
 RESULT 39
 AAP70294
 ID AAP70294 standard; protein; 281 AA.
 XX
 AC AAP70294;
 XX
 DT 25-MAR-2003 (updated)
 DT 20-MAR-1991 (first entry)
 DT


```

XX DE Subtype adr HBeAg P31.
XX KW Subtype adr HBeAg P31; vaccine; hepatitis B virus surface antigen;
XX OS Hepatitis B virus.
XX PN EP25430-A.
XX PD 09-SEP-1987.
XX PF 19-AUG-1986; 86EP-0306418.
XX PR 02-JUN-1986; 86JP-0128918.
XX PR 20-AUG-1985; 85JP-0183344.
XX PR 10-JAN-1986; 86JP-0004090.
XX PR 10-JAN-1986; 86JP-0004091.
XX PR 18-AUG-1986; 86JP-0193833.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Fujisawa Y, Itoh Y, Nishimura O, Fujit T;
XX DR WPI; 1987-251151/36.
XX PT Recombinant modified hepatitis B virus surface antigen P31
XX PT protein - used as vaccine for prevention of HBV infections and in
XX PT diagnosis
XX PS Disclosure; Fig. 2; 128pp; English.
XX CC The modified P31 protein has HBeAg activity and can bind
XX CC polymerised human serum albumin. It has been modified to render
XX CC at least one trypsin-like protease sensitive site insensitive.
XX CC It has the same biological activity as the known small particles
XX CC produced using the blood of HBV infected subjects. The modified
XX CC protein can be used in a vaccine and as an antigen for the
XX CC diagnosis of HBV infection.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 281 AA;

Query Match      88.5%; Score 54; DB 8; Length 281;
Best Local Similarity 83.3%; Pred. No. 0.032;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFSRIGDP 12
   |||||
   |||||
Db 41 PISISFSRTGDP 52

RESULT 40
AAR62870
ID AAR62870 standard; Protein; 281 AA.
XX
XX AAR62870;
XX AC
XX XX 25-MAR-2003 (updated)
XX DT 14-JUL-1995 (first entry)
XX XX
XX DE Hepatitis B Virus pres2 surface antigen.
XX XX
XX KW Hepatitis B virus; HBV; pres2 viral surface antigen; epitope;
XX KW Immunodiagnosis.
XX OS Hepatitis B Virus.
XX XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 236 /note= "Gln corresponds to CAT codon"
XX FT Misc-difference 281 /note= "Ile corresponds to AAT codon"
XX

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PN WO9425874-A1.
XX
XX PD 10-NOV-1994.
XX PF 27-APR-1994; 94WO-KR00039.
XX PR 28-APR-1993; 93KR-0007231.
XX PA (LUCK-) LUCKY CO LTD.
XX PI Cho JM, Choi DS, Choi DY, Kim CH, Kim IS, So HS,
XX PI Yang YJ;
XX DR WPI; 1994-358478/44.
XX DR P-PSDB; AAR62870.
XX PT Kit for simultaneous diagnosis of hepatitis B and C - comprising
XX PT one or more hepatitis B and C virus antigenic proteins including
XX PT one or more epitope(s)
XX PS Claim 2; Fig 7; 89pp; English.
XX CC The HBV pres2 surface antigen is a preferred antigen for use in an
XX CC immunodiagnostic kit for simultaneous detection of hepatitis C and
XX CC B viruses. The kit comprises antigenic proteins from both viruses.
XX CC The HCV protein is pref. one of KHCV CORE 14, KHCV 897, KHCV NS4E,
XX CC KHCV NS4B/NS4C or KHCV NS5-1.2 proteins; the HBV protein is pref.
XX CC HBV CORE or Pre S2 SAg protein.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 281 AA;

Query Match      88.5%; Score 54; DB 15; Length 281;
Best Local Similarity 83.3%; Pred. No. 0.032;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFSRIGDP 12
   |||||
   |||||
Db 41 PISISFSRTGDP 52

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Job time : 42 secs

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OM protein - protein search, using sw model

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Title: US-09-830-981-2

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Maximum Match 100%

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- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/6CTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/6backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	55	3 US-09-361-707-97	Sequence 97, Appl
2	61	100.0	164	4 US-09-471-573A-41	Sequence 41, Appl
3	61	100.0	174	3 US-08-480-173A-44	Sequence 44, Appl
4	61	100.0	174	3 US-08-484-408A-44	Sequence 44, Appl
5	61	100.0	281	1 US-08-105-483-214	Sequence 214, Appl
6	61	100.0	281	1 US-08-709-209-214	Sequence 214, Appl
7	61	100.0	281	1 US-08-458-101-214	Sequence 214, Appl
8	61	100.0	281	4 US-09-247-890-12	Sequence 12, Appl
9	61	100.0	281	4 US-09-724-969-12	Sequence 12, Appl
10	61	100.0	281	4 US-09-724-852-12	Sequence 12, Appl
11	61	100.0	389	1 US-08-105-483-216	Sequence 216, Appl
12	61	100.0	389	1 US-08-105-483-219	Sequence 219, Appl
13	61	100.0	389	1 US-08-709-209-216	Sequence 216, Appl
14	61	100.0	389	1 US-08-709-209-219	Sequence 219, Appl
15	61	100.0	389	1 US-08-458-101-216	Sequence 216, Appl
16	61	100.0	389	1 US-08-458-101-219	Sequence 219, Appl
17	61	100.0	389	3 US-08-486-099-106	Sequence 106, Appl
18	61	100.0	389	3 US-08-360-107A-116	Sequence 116, Appl
19	61	100.0	389	3 US-08-484-223B-106	Sequence 106, Appl
20	61	100.0	389	3 US-08-919-597-106	Sequence 106, Appl
21	61	100.0	389	3 US-08-475-668A-106	Sequence 106, Appl
22	61	100.0	389	3 US-08-485-551A-106	Sequence 106, Appl
23	61	100.0	389	3 US-08-471-913A-106	Sequence 106, Appl
24	61	100.0	389	3 US-08-485-264A-106	Sequence 106, Appl
25	61	100.0	389	4 US-08-474-349A-106	Sequence 106, Appl
26	61	100.0	389	4 US-08-470-896-106	Sequence 106, Appl
27	61	100.0	389	4 US-08-485-546A-106	Sequence 106, Appl

28	59	96.7	55	3 US-09-361-707-93	Sequence 93, Appl
29	59	96.7	55	3 US-09-361-707-95	Sequence 95, Appl
30	59	96.7	55	3 US-09-361-707-96	Sequence 96, Appl
31	59	96.7	174	2 US-08-683-262B-55	Sequence 55, Appl
32	59	96.7	174	3 US-08-480-173A-45	Sequence 45, Appl
33	59	96.7	174	3 US-08-484-408A-45	Sequence 45, Appl
34	59	96.7	174	3 US-09-361-707-55	Sequence 55, Appl
35	59	96.7	174	6 5204096-1	Patent No. 5204096
36	59	96.7	174	6 5204096-2	Patent No. 5204096
37	54	88.5	14	6 5164485-4	Patent No. 5164485
38	54	88.5	15	3 US-09-361-707-84	Sequence 84, Appl
39	54	88.5	55	3 US-09-361-707-85	Sequence 85, Appl
40	54	88.5	55	3 US-09-361-707-87	Sequence 87, Appl
41	54	88.5	55	3 US-09-361-707-89	Sequence 89, Appl
42	54	88.5	55	3 US-09-361-707-90	Sequence 90, Appl
43	54	88.5	170	2 US-08-683-262B-49	Sequence 49, Appl
44	54	88.5	170	2 US-09-361-707-49	Sequence 49, Appl
45	54	88.5	174	3 US-08-683-262B-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-361-707-97
Sequence 97, Application US/09361707
Patent No. 6258937
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
Li, Jisu
Mands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastsEq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-Jul-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-361-707-97
Query Match 100.0%; Score 61; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PLSIFSRIGDP 12
|||||
Db 41 PLSIFSRIGDP 52

RESULT 2
US-09-471-573A-41
Sequence 41, Application US/09471573A
Patent No. 6551820
GENERAL INFORMATION:
APPLICANT: Mason, Hugh
TITLE OF INVENTION: Expression of Immunogenic Hepatitis B Surface Antigens in Transge
FILE REFERENCE: 3121/1080
CURRENT APPLICATION NUMBER: US/09/471,573A
CURRENT FILING DATE: 1999-12-23
PRIORITY FILING DATE: 1998-12-23
PRIORITY FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 41
LENGTH: 164
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Plant optimized pre-S (pre-S1/S2) amino acid sequence
NAME/KEY: misc feature
OTHER INFORMATION: Plant optimized pre-S (pre-S1/S2) amino acid sequence
US-09-471-573A-41

Query Match 100.0%; Score 61; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRRIGDP 12
DB 149 PLSISFRRIGDP 160

RESULT 3
US-08-480-173A-44
Sequence 44, Application US/08480173A
Patent No. 6072049
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Miles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8991
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-480-173A-44

Query Match 100.0%; Score 61; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRRIGDP 12
DB 160 PLSISFRRIGDP 171

RESULT 4
US-08-484-408A-44
Sequence 44, Application US/08484408A
Patent No. 6117653
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Miles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8991
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-408A-44

Query Match 100.0%; Score 61; DB 3; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRRIGDP 12
DB 160 PLSISFRRIGDP 171

RESULT 5
US-08-105-483-214
Sequence 214, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Paolletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford

```

/ ADDRESSSEE: c/o William S. Frommer
/ STREET: 530 Fifth Avenue
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/105,483
/ FILING DATE: 12-AUG-1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/847,951
/ FILING DATE: 06-MAR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Frommer, William S.
/ REGISTRATION NUMBER: 25,506
/ REFERENCE/DOCKET NUMBER: 454310-2400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 840-3333
/ TELEFAX: (212) 840-0712
/ INFORMATION FOR SEQ ID NO: 214:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 281 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-105-483-214

Query Match      100.0%; Score 61; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLSISFRRIGDP 12
DB      41 PLSISFRRIGDP 52

RESULT 6
US-08-709-209-214
/ Sequence 214: Application US/08709209
/ Patent No. 5762938
/ GENERAL INFORMATION:
/ APPLICANT: Paolletti, Enzo
/ TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
/ TITLE OF INVENTION: STRAIN
/ NUMBER OF SEQUENCES: 462
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Curtis, Morris & Safford
/ STREET: 530 Fifth Avenue
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/709,209
/ FILING DATE: 21-AUG-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/105,483
/ FILING DATE: 12-AUG-1993
/ APPLICATION NUMBER: US 07/847,951
/ FILING DATE: 06-MAR-1992
/
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```

/ ATTORNEY/AGENT INFORMATION:
/ NAME: Frommer, William S.
/ REGISTRATION NUMBER: 25,506
/ REFERENCE/DOCKET NUMBER: 454310-2400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 840-3333
/ TELEFAX: (212) 840-0712
/ INFORMATION FOR SEQ ID NO: 214:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 281 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-709-209-214

Query Match      100.0%; Score 61; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLSISFRRIGDP 12
DB      41 PLSISFRRIGDP 52

RESULT 7
US-08-458-101-214
/ Sequence 214: Application US/08458101
/ Patent No. 5765939
/ GENERAL INFORMATION:
/ APPLICANT: Paolletti, Enzo
/ APPLICANT: Perkus, Marion E.
/ APPLICANT: Taylor, Jill
/ APPLICANT: Tartaglia, James
/ APPLICANT: No. 5766590cn, Elizabeth K.
/ APPLICANT: Riviere, Michel
/ APPLICANT: de Taisne, Charles
/ APPLICANT: Limbach, Keith J.
/ APPLICANT: Johnson, Gerard P.
/ APPLICANT: Pincus, Steven E.
/ APPLICANT: Cox, William I.
/ APPLICANT: Audonnet, Jean-Christophe
/ APPLICANT: Gettys, Russell Robert
/ TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
/ TITLE OF INVENTION: STRAIN
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Curtis, Morris & Safford
/ STREET: 530 Fifth Avenue
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/458,101
/ FILING DATE: 01-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Frommer, William S.
/ REGISTRATION NUMBER: 25,506
/ REFERENCE/DOCKET NUMBER: 454310-2740
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 840-3333
/ TELEFAX: (212) 840-0712
/ INFORMATION FOR SEQ ID NO: 214:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 281 amino acids
/ TYPE: amino acid
/
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STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-214

Query Match 100.0%; Score 61; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
|||||
Db 41 PLSSTFSRIGDP 52

RESULT 8
US-09-247-890-12
Sequence 12, Application US/09247890
Patent No. 6541011
GENERAL INFORMATION:
APPLICANT: Punnonen, Juha
APPLICANT: Baas, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/247, 890
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: US 60/074,294
EARLIER FILING DATE: 1998-02-11
EARLIER APPLICATION NUMBER: US 60/105,509
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 281
TYPE: PRT
ORGANISM: Hepatitis B virus
US-09-247-890-12

Query Match 100.0%; Score 61; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
|||||
Db 41 PLSSTFSRIGDP 52

RESULT 9
US-09-724-969-12
Sequence 12, Application US/09724969
Patent No. 6569435
GENERAL INFORMATION:
APPLICANT: Punnonen, Juha
APPLICANT: Baas, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/724, 969
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/247, 890
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: US 60/105,509
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 281
TYPE: PRT

ORGANISM: Hepatitis B virus
US-09-724-969-12

Query Match 100.0%; Score 61; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
|||||
Db 41 PLSSTFSRIGDP 52

RESULT 10
US-09-724-852-12
Sequence 12, Application US/09724852
Patent No. 6576757
GENERAL INFORMATION:
APPLICANT: Punnonen, Juha
APPLICANT: Baas, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/724, 852
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/09/247, 890
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 281
TYPE: PRT
ORGANISM: Hepatitis B virus
US-09-724-852-12

Query Match 100.0%; Score 61; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
|||||
Db 41 PLSSTFSRIGDP 52

RESULT 11
US-08-105-483-216
Sequence 216, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Paolletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESS: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-216

Query Match 100.0%; Score 61; DB 1; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
DB 149 PLSIFSRIGDP 160

RESULT 12
US-08-105-483-219
Sequence 219, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-219

Query Match 100.0%; Score 61; DB 1; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
DB 149 PLSIFSRIGDP 160

RESULT 13
US-08-709-209-216
Sequence 216, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-209-216

Query Match 100.0%; Score 61; DB 1; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
DB 149 PLSIFSRIGDP 160

RESULT 14
US-08-709-209-219
Sequence 219, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN

NUMBER OF SEQUENCES: 462
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 ADDRESSEE: c/o William S. Frommer
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,209
 FILING DATE: 21-AUG-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/105,483
 FILING DATE: 12-AUG-1993
 APPLICATION NUMBER: US 07/847,951
 FILING DATE: 06-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 219:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-709-209-219

Query Match 100.0%; Score 61; DB 1; Length 389;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
 |||||
 DB 149 PLSIFSRIGDP 160

RESULT 15
 US-08-458-101-216
 Sequence 216, Application US/08458101
 Patent No. 5766599
 GENERAL INFORMATION:
 APPLICANT: Paoletti, Enzo
 APPLICANT: Perkus, Marion E.
 APPLICANT: Taylor, Jill
 APPLICANT: Tartaglia, James
 APPLICANT: No. 5766599ton, Elizabeth K.
 APPLICANT: Riviere, Michel
 APPLICANT: de Taisne, Charles
 APPLICANT: Limbach, Keith J.
 APPLICANT: Johnson, Gerard P.
 APPLICANT: Pincus, Steven E.
 APPLICANT: Cox, William I.
 APPLICANT: Audonnet, Jean-Christophe
 APPLICANT: Gettig, Russell Robert
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 ADDRESSEE: c/o William S. Frommer
 STREET: 530 Fifth Avenue
 CITY: New York

STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,101
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2740
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 216:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-458-101-216

Query Match 100.0%; Score 61; DB 1; Length 389;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
 |||||
 DB 149 PLSIFSRIGDP 160

RESULT 16
 US-08-458-101-219
 Sequence 219, Application US/08458101
 Patent No. 5766599
 GENERAL INFORMATION:
 APPLICANT: Paoletti, Enzo
 APPLICANT: Perkus, Marion E.
 APPLICANT: Taylor, Jill
 APPLICANT: Tartaglia, James
 APPLICANT: No. 5766599ton, Elizabeth K.
 APPLICANT: Riviere, Michel
 APPLICANT: de Taisne, Charles
 APPLICANT: Limbach, Keith J.
 APPLICANT: Johnson, Gerard P.
 APPLICANT: Pincus, Steven E.
 APPLICANT: Cox, William I.
 APPLICANT: Audonnet, Jean-Christophe
 APPLICANT: Gettig, Russell Robert
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 ADDRESSEE: c/o William S. Frommer
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,101
 FILING DATE: 01-JUN-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-219

Query Match 100.0%; Score 61; DB 1; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
Db 149 PLSIFSRIGDP 160

RESULT 17
US-08-486-099-106
Sequence 106, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
US-08-486-099-106

Query Match 100.0%; Score 61; DB 3; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
Db 149 PLSIFSRIGDP 160

RESULT 18
US-08-360-107A-116
Sequence 116, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
US-08-360-107A-116

Query Match 100.0%; Score 61; DB 3; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
Db 149 PLSIFSRIGDP 160

RESULT 19
US-08-484-223B-106
Sequence 106, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223B-106

Query Match 100.0%; Score 61; DB 3; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
Db 149 PLSIFSRIGDP 160

RESULT 20
US-08-919-597-106
Sequence 106, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-106

Query Match 100.0%; Score 61; DB 3; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
Db 149 PLSIFSRIGDP 160

RESULT 21
US-08-475-668A-106
Sequence 106, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-106

Query Match 100.0%; Score 61; DB 3; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSISFRIGDP 12
Db 149 PLSISFRIGDP 160

RESULT 22
US-08-485-551A-106
Sequence 106, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-106

Query Match 100.0%; Score 61; DB 3; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSISFRIGDP 12
Db 149 PLSISFRIGDP 160

RESULT 23
US-08-471-913A-106
Sequence 106, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-106

Query Match 100.0%; Score 61; DB 3; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSISFRIGDP 12
Db 149 PLSISFRIGDP 160

RESULT 24
US-08-485-264A-106
Sequence 106, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-106

Query Match 100.0%; Score 61; DB 3; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
DB 149 PLSIFSRIGDP 160

RESULT 25
US-08-474-349A-106
Sequence 106, Application US/0847349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-474-349A-106

Query Match 100.0%; Score 61; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
DB 149 PLSIFSRIGDP 160

RESULT 26
US-08-470-896-106
Sequence 106, Application US/08470896
Patent No. 6479055
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-896-106

Query Match 100.0%; Score 61; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFRIQDP 12
Db 149 PLSISFRIQDP 160

RESULT 27

US-08-485-546A-106
Sequence 106, Application US/08485546A
Patent No. 6518013

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-106

Query Match 100.0%; Score 61; DB 4; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFRIQDP 12
Db 149 PLSISFRIQDP 160

RESULT 28

US-09-361-707-93
Sequence 93, Application US/09361707
Patent No. 6258937

GENERAL INFORMATION:
APPLICANT: Tong, Shuping
NAME: Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-JUL-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-361-707-93

Query Match 96.7%; Score 59; DB 3; Length 55;
Best Local Similarity 91.7%; Pred. No. 0.00028;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFRIQDP 12
Db 41 PLSISFRIQDP 52

RESULT 29

US-09-361-707-95
Sequence 95, Application US/09361707
Patent No. 6258937

GENERAL INFORMATION:
APPLICANT: Tong, Shuping
NAME: Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-Jul-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-361-707-95

Query Match 96.7%; Score 59; DB 3; Length 55;
Best Local Similarity 91.7%; Pred. No. 0.00028;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIQDP 12
Db 41 PLSIFSRIQDP 52

RESULT 30
US-09-361-707-96
Sequence 96, Application US/09361707
Patent No. 6258937
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
L.I. Jie
Mands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-Jul-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:

LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-361-707-96

Query Match 96.7%; Score 59; DB 3; Length 55;
Best Local Similarity 91.7%; Pred. No. 0.00028;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIQDP 12
Db 41 PLSIFSRIQDP 52

RESULT 31
US-08-683-262B-55
Sequence 55, Application US/08683262B
Patent No. 5929220
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,262B
FILING DATE: 18-Jul-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-262B-55

Query Match 96.7%; Score 59; DB 2; Length 174;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIQDP 12
Db 160 PLSIFSRIQDP 171

RESULT 32
US-08-480-173A-45
Sequence 45, Application US/08480173A
Patent No. 6072049
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:

ADDRESSEE: Popovich & Miles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8991
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-480-173A-45

Query Match 96.7%; Score 59; DB 3; Length 174;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PUSISFRRIGDP 12
Db 160 PISISFRRIGDP 171

RESULT 33
US-08-484-408A-45
Sequence 45, Application US/08484408A
Patent No. 6117653
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Miles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-334-8991
TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-408A-45

Query Match 96.7%; Score 59; DB 3; Length 174;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PUSISFRRIGDP 12
Db 160 PISISFRRIGDP 171

RESULT 34
US-09-361-707-55
Sequence 55, Application US/09361707
Patent No. 6258937
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
L1, Jisu
Wande, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 55:

US-09-361-707-55

Query Match 96.7%; Score 59; DB 3; Length 174;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PUSISFRRIGDP 12
Db 160 PISISFRRIGDP 171

RESULT 35
5204096-1
Patent No. 5204096
APPLICANT: NEURATH, ALEXANDER R.; KENT, B.H.

TITLE OF INVENTION: PRE-S GENE CODED PEPTIDE HEPATITIS B
IMMUNOGENS, VACCINES, DIAGNOSTICS, AND SYNTHETIC LIPID VESICLE
CARRIERS
NUMBER OF SEQUENCES: 36
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/338,028
FILING DATE: 14-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 698,499
FILING DATE: 05-FEB-1985
APPLICATION NUMBER: 587,090
FILING DATE: 07-MAR-1984
SEQ ID NO: 1:
LENGTH: 174
5204096-1

Query Match 96.7%; Score 59; DB 6; Length 174;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRTGDP 12
|:|||||
Db 160 PLSISFRTGDP 171

RESULT 36
5204096-2
Patent No. 5204096
APPLICANT: NEURATH, ALEXANDER R.; KENT, B.H.
TITLE OF INVENTION: PRE-S GENE CODED PEPTIDE HEPATITIS B
IMMUNOGENS, VACCINES, DIAGNOSTICS, AND SYNTHETIC LIPID VESICLE
CARRIERS
NUMBER OF SEQUENCES: 36
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/338,028
FILING DATE: 14-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 698,499
FILING DATE: 05-FEB-1985
APPLICATION NUMBER: 587,090
FILING DATE: 07-MAR-1984
SEQ ID NO: 2:
LENGTH: 174
5204096-2

Query Match 96.7%; Score 59; DB 6; Length 174;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRTGDP 12
|:|||||
Db 160 PLSISFRTGDP 171

RESULT 37
5164485-4
Patent No. 5164485
APPLICANT: FUJISAWA, YUKIO; ITOH, YASUAKI; NISHIMURA, OSAMU
FUJII, TOMOYO
TITLE OF INVENTION: MODIFIED HEPATITIS B VIRUS SURFACE
ANTIGEN P31 AND PRODUCTION THEREOF
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/547,948
FILING DATE: 03-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 898,425
FILING DATE: 20-AUG-1986
SEQ ID NO: 4:
LENGTH: 14
5164485-4

Query Match 88.5%; Score 54; DB 6; Length 14;

Best Local Similarity 83.3%; Pred. No. 0.00052;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFRTGDP 12
|:|||||
Db 1 PLSISFRTGDP 12

RESULT 38
US-09-361-707-84
Sequence 84, Application US/09361707
Patent No. 6258937
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
Li, Jisu
Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSQ for windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-09-361-707-84

Query Match 88.5%; Score 54; DB 3; Length 55;
Best Local Similarity 83.3%; Pred. No. 0.0025;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFRTGDP 12
|:|||||
Db 41 PLSISFRTGDP 52

RESULT 39
US-09-361-707-85
Sequence 85, Application US/09361707
Patent No. 6258937
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
Li, Jisu
Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-Jul-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-09-361-707-85

Query Match 88.5%; Score 54; DB 3; Length 55;
Best Local Similarity 83.3%; Pred. No. 0.0025;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFSRIGDP 12
|:|||||
Db 41 PLSISFSRIGDP 52

RESULT 40
US-09-361-707-87
Sequence 87, Application US/09361707
Patent No. 6258937
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
L1, Jisu
Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-Jul-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-09-361-707-87

Query Match 88.5%; Score 54; DB 3; Length 55;
Best Local Similarity 83.3%; Pred. No. 0.0025;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFSRIGDP 12
|:|||||
Db 41 PLSISFSRIGDP 52

Search completed: November 6, 2003, 15:13:49
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: November 6, 2003, 15:12:49 ; Search time 29 Seconds
(without alignments)
71.069 Million cell updates/sec

Title: US-09-830-981-2

Perfect score: 61

Sequence: 1 PLSISFRIGDP 12

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	12	15	US-10-226-956-284
2	61	100.0	12	15	US-10-077-555-9
3	61	100.0	12	15	US-10-211-088-302
4	61	100.0	12	10	US-09-247-890-12
5	59	96.7	174	9	US-09-818-066-55
6	59	96.7	389	10	US-09-821-877-2
7	54	88.5	170	9	US-09-818-066-49
8	54	88.5	174	9	US-09-818-066-46
9	54	88.5	174	9	US-09-818-066-48
10	54	88.5	174	9	US-09-818-066-56
11	54	88.5	281	10	US-09-247-890-10
12	54	88.5	400	15	US-10-209-284-3
13	52	85.2	174	9	US-09-818-066-50
14	52	85.2	174	9	US-09-818-066-58
15	52	85.2	389	16	US-10-169-668-6

16	49	80.3	174	9	US-09-818-066-53	Sequence 53, Appl
17	46	75.4	174	9	US-09-818-066-45	Sequence 45, Appl
18	46	75.4	174	9	US-09-818-066-47	Sequence 47, Appl
19	44	72.1	174	9	US-09-818-066-37	Sequence 37, Appl
20	44	72.1	174	9	US-09-818-066-54	Sequence 54, Appl
21	43	70.5	174	9	US-09-818-066-57	Sequence 57, Appl
22	40	65.6	64	9	US-09-917-340-85	Sequence 85, Appl
23	40	65.6	64	15	US-10-157-031-118	Sequence 118, App
24	40	65.6	174	9	US-09-818-066-62	Sequence 42, Appl
25	40	65.6	174	9	US-09-818-066-62	Sequence 62, Appl
26	38	62.3	174	9	US-09-818-066-38	Sequence 38, Appl
27	38	62.3	174	9	US-09-818-066-40	Sequence 40, Appl
28	37	60.7	174	9	US-09-818-066-41	Sequence 41, Appl
29	37	60.7	174	9	US-09-818-066-59	Sequence 59, Appl
30	37	60.7	217	12	US-10-291-190-42	Sequence 42, Appl
31	36.5	59.8	335	12	US-09-995-938A-8	Sequence 8, Appl
32	36.5	59.8	335	12	US-09-995-938A-10	Sequence 10, Appl
33	36	59.0	55	9	US-09-879-257A-45	Sequence 45, Appl
34	36	59.0	174	9	US-09-818-066-35	Sequence 35, Appl
35	36	59.0	174	9	US-09-818-066-36	Sequence 36, Appl
36	36	59.0	174	9	US-09-818-066-52	Sequence 52, Appl
37	36	59.0	174	16	US-10-169-668-4	Sequence 4, Appl
38	35	57.4	96	9	US-09-864-761-39796	Sequence 39796, A
39	35	57.4	110	15	US-10-106-698-6697	Sequence 6697, Ap
40	35	57.4	173	12	US-10-205-979-48	Sequence 48, Appl
41	35	57.4	173	14	US-10-051-663-207	Sequence 207, App
42	35	57.4	174	9	US-09-818-066-39	Sequence 39, Appl
43	35	57.4	400	12	US-10-224-999A-3461	Sequence 3461, Ap
44	35	57.4	613	15	US-10-156-761-13218	Sequence 13218, A
45	35	57.4	690	9	US-09-815-242-12460	Sequence 12460, A

ALIGNMENTS

RESULT 1
US-10-226-956-284
; Sequence 284, Application US/10226956
; Publication No. US20030060399A1
GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilaa, Padmini
; APPLICANT: Pantich, Alyssa
; APPLICANT: Joshi, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: ASU-1061-US
; CURRENT APPLICATION NUMBER: US/10/226,956
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 284
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-226-956-284
Query Match 100.0%; Score 61; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLSISFRIGDP 12
|||
Db 1 PLSISFRIGDP 12
RESULT 2
US-10-077-555-9
; Sequence 9, Application US/10077555

```
/ Publication No. US20030077289A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Rong-fu
/ TITLE OF INVENTION: Use of Cell-Penetrating Peptides to Generate Antitumor Immunity
/ FILE REFERENCE: P02373US1/10200806
/ CURRENT APPLICATION NUMBER: US/10/077,555
/ PRIOR FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: US 60/268,687
/ PRIOR FILING DATE: 2001-02-15
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 9
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Hepatitis B virus
US-10-077-555-9

Query Match          100.0%; Score 61; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7,1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLSISFRRIGDP 12
        |||||
        1 PLSISFRRIGDP 12

Db

RESULT 3
US-10-211-088-302
/ Sequence 302, Application US/10211088
/ Publication No. US20030104479A1
/ GENERAL INFORMATION:
/ APPLICANT: Bright, Gary R.
/ APPLICANT: Premkumar, D. David
/ APPLICANT: Chen, Yih-Tai
/ TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular Bi
/ FILE REFERENCE: 01-1022-US
/ CURRENT APPLICATION NUMBER: US/10/211,088
/ PRIOR FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: 60/309,395
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/341,589
/ PRIOR FILING DATE: 2001-12-13
/ NUMBER OF SEQ ID NOS: 366
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 302
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Protein-derived transport peptide
US-10-211-088-302

Query Match          100.0%; Score 61; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7,1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLSISFRRIGDP 12
        |||||
        1 PLSISFRRIGDP 12

Db

RESULT 4
US-09-247-890-12
/ Sequence 12, Application US/09247890
/ Publication No. US20020198162A1
/ GENERAL INFORMATION:
/ APPLICANT: Punnonen, Juha
/ APPLICANT: Baas, Steven H.
/ APPLICANT: Whalen, Robert Gerald
/ APPLICANT: Howard, Russell
/ APPLICANT: Stemmer, Willem P.C.
/ APPLICANT: Maxygen, Inc.
/ TITLE OF INVENTION: Antigen Library Immunization
```

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/ FILE REFERENCE: 018097-028710US
/ CURRENT APPLICATION NUMBER: US/09/247,890
/ CURRENT FILING DATE: 1999-02-10
/ EARLIER APPLICATION NUMBER: US 60/074,294
/ EARLIER FILING DATE: 1998-02-11
/ EARLIER APPLICATION NUMBER: US 60/105,509
/ EARLIER FILING DATE: 1998-10-23
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 281
/ TYPE: PRT
/ ORGANISM: Hepatitis B virus
US-09-247-890-12

Query Match          100.0%; Score 61; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLSISFRRIGDP 12
        |||||
        41 PLSISFRRIGDP 52

Db

RESULT 5
US-09-818-066-55
/ Sequence 55, Application US/09818066
/ Patent No. US20020032307A1
/ GENERAL INFORMATION:
/ APPLICANT: Shuping Tong et al.
/ TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
/ NUMBER OF SEQUENCES: 75
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/818,066
/ FILING DATE: 27-Mar-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/683,262
/ FILING DATE: 18-Jul-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 31,819
/ REFERENCE/DOCKET NUMBER: 00786/287002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 55:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 174 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-818-066-55

Query Match          96.7%; Score 59; DB 9; Length 174;
Best Local Similarity 91.7%; Pred. No. 0.0031;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 PLSISFRRIGDP 12
```

Db 160 PISSTFSRIGDP 171

|||||

RESULT 6

US-09-821-877-2

Sequence 2, Application US/09821877

Patent No. US20020177124A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Coleman, Paul F.

APPLICANT: Mushahwar, Isa K.

TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant

TITLE OF INVENTION: And Methods Of Detection Thereof

FILE REFERENCE: 6794 US 01

CURRENT APPLICATION NUMBER: US/09/821,877

CURRENT FILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 2

LENGTH: 389

TYPE: PRT

ORGANISM: Hepatitis B Virus

US-09-821-877-2

Query Match

Best Local Similarity 96.7%; Score 59; DB 10; Length 389;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12

|||||

Db 149 PISSTFSRIGDP 160

RESULT 7

US-09-818-066-49

Sequence 49, Application US/09818066

Patent No. US20020032307A1

GENERAL INFORMATION:

APPLICANT: Shuping Tong et al.

TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/818,066

FILING DATE: 27-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/683,262

FILING DATE: 18-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 31,819

REFERENCE/DOCKET NUMBER: 00786/287002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 49:

US-09-818-066-49

Query Match

Best Local Similarity 83.3%; Score 54; DB 9; Length 174;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12

|||||

Db 160 PISSTFSRIGDP 171

RESULT 8

US-09-818-066-46

Sequence 46, Application US/09818066

Patent No. US20020032307A1

GENERAL INFORMATION:

APPLICANT: Shuping Tong et al.

TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/818,066

FILING DATE: 27-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/683,262

FILING DATE: 18-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 31,819

REFERENCE/DOCKET NUMBER: 00786/287002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-09-818-066-46

Query Match

Best Local Similarity 88.5%; Score 54; DB 9; Length 174;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12

|||||

Db 160 PISSTFSRIGDP 171

RESULT 9

US-09-818-066-48

Sequence 48, Application US/09818066

Patent No. US20020032307A1

GENERAL INFORMATION:

APPLICANT: Shuping Tong et al.

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 49:

US-09-818-066-49

Query Match

Best Local Similarity 88.5%; Score 54; DB 9; Length 170;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12

|||||

Db 156 PISSTFSRIGDP 167

RESULT 8

US-09-818-066-46

Sequence 46, Application US/09818066

Patent No. US20020032307A1

GENERAL INFORMATION:

APPLICANT: Shuping Tong et al.

TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/818,066

FILING DATE: 27-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/683,262

FILING DATE: 18-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 31,819

REFERENCE/DOCKET NUMBER: 00786/287002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-09-818-066-46

Query Match

Best Local Similarity 88.5%; Score 54; DB 9; Length 174;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12

|||||

Db 160 PISSTFSRIGDP 171

RESULT 9

US-09-818-066-48

Sequence 48, Application US/09818066

Patent No. US20020032307A1

GENERAL INFORMATION:

APPLICANT: Shuping Tong et al.

TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-818-066-48
Query Match 88.5%; Score 54; DB 9; Length 174;
Best Local Similarity 83.3%; Pred. No. 0.026; 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLSIFSRIGDP 12
Db 160 PLSIFSRIGDP 171
RESULT 10
US-09-818-066-56
Sequence 56; Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262

FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-818-066-56
Query Match 88.5%; Score 54; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.026; 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLSIFSRIGD 11
Db 160 PLSIFSRIGD 170
RESULT 11
US-09-247-890-10
Sequence 10; Application US/09247890
Publication No. US20020198162A1
GENERAL INFORMATION:
APPLICANT: Punnonen, Juha
APPLICANT: Baes, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/247,890
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: US 60/074,294
EARLIER FILING DATE: 1998-02-11
EARLIER APPLICATION NUMBER: US 60/105,509
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 281
TYPE: PRT
ORGANISM: Hepatitis B virus
US-09-247-890-10
Query Match 88.5%; Score 54; DB 10; Length 281;
Best Local Similarity 83.3%; Pred. No. 0.044; 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLSIFSRIGDP 12
Db 41 PLSIFSRIGDP 52
RESULT 12
US-10-209-264-3
Sequence 3; Application US/10209264
Publication No. US20030003111A1
GENERAL INFORMATION:
APPLICANT: Oon, Chong Jin
Lim, Gek Keow
Zhao, Yi
Chen, Wei Ning
TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND

USERS THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ladae & Parry

STREET: 26 West 61 Street

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10023

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/209,264

FILING DATE: 31-Jul-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/SG98/00046

FILING DATE: 19-Jan-1998

ATTORNEY/AGENT INFORMATION:

NAME: Mass, Clifford J.

REGISTRATION NUMBER: 30,086

REFERENCE/DOCKET NUMBER: U-013109-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 708-1800

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-209-264-3

Query Match

Best Local Similarity 88.5%; Score 54; DB 15; Length 400;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12

Db 160 PLSIFSRIGDP 171

RESULT 13

US-09-818-066-50

Sequence 50, Application US/09818066

Patent No. US20020032307A1

GENERAL INFORMATION:

APPLICANT: Shuping Tong et al.

TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/818,066

FILING DATE: 27-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/683,262

FILING DATE: 18-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 31,819

REFERENCE/DOCKET NUMBER: 00786/287002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-09-818-066-50

Query Match

Best Local Similarity 85.2%; Score 52; DB 9; Length 174;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISSIFSRIGDP 12

Db 161 ISSIFSRIGDP 171

RESULT 14

US-09-818-066-58

Sequence 58, Application US/09818066

Patent No. US20020032307A1

GENERAL INFORMATION:

APPLICANT: Shuping Tong et al.

TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/818,066

FILING DATE: 27-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/683,262

FILING DATE: 18-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 31,819

REFERENCE/DOCKET NUMBER: 00786/287002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-09-818-066-58

Query Match

Best Local Similarity 85.2%; Score 52; DB 9; Length 174;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
 DB 161 ISSIFSRIGDP 171

RESULT 15

US-10-169-668-6
 ; Sequence 6, Application US/10169668
 ; Publication No. US20030129202A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BIOMERIEUX
 ; APPLICANT: INSEEM
 ; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
 ; FILE REFERENCE: IFB 99 INS HBVM
 ; CURRENT APPLICATION NUMBER: US/10/169,668
 ; CURRENT FILING DATE: 2002-07-08
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 389
 ; TYPE: PRT
 ; ORGANISM: mutated hepatitis B virus mHBV
 US-10-169-668-6

Query Match 85.2%; Score 52; DB 16; Length 389;
 Best Local Similarity 90.9%; Pred. No. 0.15;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
 DB 150 ISSIFSRIGDP 160

RESULT 16

US-09-818-066-53
 ; Sequence 53, Application US/09818066
 ; Patent No. US20020032307A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shuping Tong et al.
 ; TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
 ; NUMBER OF SEQUENCES: 75
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/818,066
 ; FILING DATE: 27-Mar-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/683,262
 ; FILING DATE: 18-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Frazer, Janis K.
 ; REGISTRATION NUMBER: 31,819
 ; REFERENCE/DOCKET NUMBER: 00786/287002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 174 amino acids
 ; TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 53:
 US-09-818-066-53

Query Match 80.3%; Score 49; DB 9; Length 174;
 Best Local Similarity 81.8%; Pred. No. 0.23;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
 DB 161 ISSIFSRIGDP 171

RESULT 17

US-09-818-066-45
 ; Sequence 45, Application US/09818066
 ; Patent No. US20020032307A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shuping Tong et al.
 ; TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
 ; NUMBER OF SEQUENCES: 75
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/818,066
 ; FILING DATE: 27-Mar-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/683,262
 ; FILING DATE: 18-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Frazer, Janis K.
 ; REGISTRATION NUMBER: 31,819
 ; REFERENCE/DOCKET NUMBER: 00786/287002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 174 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
 US-09-818-066-45

Query Match 75.4%; Score 46; DB 9; Length 174;
 Best Local Similarity 75.0%; Pred. No. 0.83;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSSIFSRIGDP 12
 DB 160 PISISSRIGDP 171

RESULT 18

US-09-818-066-47
 ; Sequence 47, Application US/09818066
 ; Patent No. US20020032307A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shuping Tong et al.

TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-818-066-47

Query Match 75.4%; Score 46; DB 9; Length 174;
Best Local Similarity 75.0%; Pred. No. 0.83;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
Db 160 PLSISSRTGDP 171

RESULT 19
US-09-818-066-37
Sequence 37, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262

FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-818-066-37

Query Match 72.1%; Score 44; DB 9; Length 174;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LSSIFSRIGDP 12
Db 161 ISSISSRTGDP 171

RESULT 20
US-09-818-066-54
Sequence 54, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-818-066-54

Query Match 72.1%; Score 44; DB 9; Length 174;
Best Local Similarity 75.0%; Pred. No. 2;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PLSISFRIGDP 12
|:|||||
Db 160 PLSISFRITDP 171

RESULT 21
US-09-818-066-57
; Sequence 57, Application US/09818066
; Patent No. US20020032307A1
; GENERAL INFORMATION:
; APPLICANT: Shuping Tong et al.
; TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-818-066-57

Query Match 70.5%; Score 43; DB 9; Length 174;
Best Local Similarity 72.7%; Pred. No. 3;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 11
|:|||||
Db 160 PLSISFRITDP 170

RESULT 22
US-09-917-340-85
; Sequence 85, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632

; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 85
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-85

Query Match 65.6%; Score 40; DB 9; Length 64;
Best Local Similarity 58.3%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 12
|:|||||
Db 17 PLPGVFGIGDP 28

RESULT 23
US-10-157-031-118
; Sequence 118, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 118
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-118

Query Match 65.6%; Score 40; DB 15; Length 64;
Best Local Similarity 58.3%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 12
|:|||||
Db 17 PLPGVFGIGDP 28

RESULT 24
US-09-818-066-42
; Sequence 42, Application US/09818066
; Patent No. US20020032307A1
; GENERAL INFORMATION:
; APPLICANT: Shuping Tong et al.
; TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-818-066-42

Query Match 65.6%; Score 40; DB 9; Length 174;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 USSIFSRIGDP 12
DB 160 PISTRESRTGDP 171

RESULT 25
US-09-818-066-62
Sequence 62, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-818-066-62

Query Match 65.6%; Score 40; DB 9; Length 174;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 USSIFSRIGDP 12
DB 161 ISSVFTSGTDP 171

RESULT 26
US-09-818-066-38
Sequence 38, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-818-066-38

Query Match 62.3%; Score 38; DB 9; Length 174;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 USSIFSRIGDP 12
DB 161 ISSVFTSGTDP 171

RESULT 27
US-09-818-066-40
Sequence 40, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR

NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-818-066-40
Query Match 62.3%; Score 38; DB 9; Length 174;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LSIIFSRIGDP 12
DB 161 ISSILSKTGP 171
RESULT 28
US-09-818-066-41
Sequence 41, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-818-066-41
Query Match 62.3%; Score 38; DB 9; Length 174;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LSIIFSRIGDP 12
DB 161 ISSILSKTGP 171
RESULT 29
US-09-818-066-59
Sequence 59, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-818-066-59
Query Match 60.7%; Score 37; DB 9; Length 174;
Best Local Similarity 72.7%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSIFSRIGDP 12
:|||||
Db 161 ISSIFSRITDP 171

RESULT 30
US-10-291-190-42
; Sequence 42, Application US/10291190
; Publication No. US20030171549A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomics, Inc.
; APPLICANT: Park, Frances
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF YIIM PROTEINS
; FILE REFERENCE: 52498-20009.00
; CURRENT APPLICATION NUMBER: US/10/291,190
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/337,769
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 217
; TYPE: PRT
; ORGANISM: A. tumefaciens (15887448)
US-10-291-190-42

Query Match 60.7%; Score 37; DB 12; Length 217;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
:|:::|
Db 129 PCATLSARIGDP 140

RESULT 31
US-09-995-938A-8
; Sequence 8, Application US/09995938A
; Publication No. US20030150026A1
; GENERAL INFORMATION:
; APPLICANT: JOANNE CHORY
; APPLICANT: ZHIYONG WANG
; TITLE OF INVENTION: GENES INVOLVED IN BRASSINOSTEROID
; TITLE OF INVENTION: HORMONE ACTION IN PLANTS
; FILE REFERENCE: SALKINS.046A
; CURRENT APPLICATION NUMBER: US/09/995,938A
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 335
; TYPE: PRT
; ORGANISM: ARABIDOPSIS THALIANA
US-09-995-938A-8

Query Match 59.8%; Score 36.5; DB 12; Length 335;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 PLSIF--SRIGDP 12
|:|:|:|
Db 130 PSSSFPSPSRVGD 144

RESULT 32
US-09-995-938A-10
; Sequence 10, Application US/09995938A
; Publication No. US20030150026A1
; GENERAL INFORMATION:

; APPLICANT: JOANNE CHORY
; APPLICANT: ZHIYONG WANG
; TITLE OF INVENTION: GENES INVOLVED IN BRASSINOSTEROID
; TITLE OF INVENTION: HORMONE ACTION IN PLANTS
; FILE REFERENCE: SALKINS.046A
; CURRENT APPLICATION NUMBER: US/09/995,938A
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 335
; TYPE: PRT
; ORGANISM: ARABIDOPSIS THALIANA
US-09-995-938A-10

Query Match 59.8%; Score 36.5; DB 12; Length 335;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 PLSIF--SRIGDP 12
|:|:|:|
Db 130 PSSSFPSPSRVGD 144

RESULT 33
US-09-879-257A-45
; Sequence 45, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORO
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Hepatitis B Virus
US-09-879-257A-45

Query Match 59.0%; Score 36; DB 9; Length 55;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISSIFSRIGDP 12
:|||||
Db 42 ISSISARTGDP 52

RESULT 34
US-09-818-066-35
; Sequence 35, Application US/09818066
; Patent No. US20020032307A1
; GENERAL INFORMATION:
; APPLICANT: Shuping Tong et al.
; TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

;
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/818,066
;   FILING DATE: 27-Mar-2001
;   CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/683,262
;   FILING DATE: 18-JUL-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fraser, Janis K.
;     REGISTRATION NUMBER: 31,819
;   REFERENCE/DOCKET NUMBER: 00786/287002
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 542-5070
;     TELEFAX: (617) 542-8906
;     TELEX: 200154
;
; INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 174 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 35:
;
; US-09-818-066-35
;
Query Match          59.0%; Score 36; DB 9; Length 174;
Best Local Similarity 63.6%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 LSSIFSRIGDP 12
Db      161 ISSISARTGDP 171

RESULT 35
; US-09-818-066-36
; Sequence 36, Application US/09818066
; Patent No. US20020032307A1
; GENERAL INFORMATION:
;   APPLICANT: Shuping Tong et al.
;   TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
;   NUMBER OF SEQUENCES: 75
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: Fish & Richardson P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: U.S.A.
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/818,066
;     FILING DATE: 27-Mar-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/683,262
;     FILING DATE: 18-JUL-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Fraser, Janis K.
;       REGISTRATION NUMBER: 31,819
;     REFERENCE/DOCKET NUMBER: 00786/287002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (617) 542-5070
;       TELEFAX: (617) 542-8906
;       TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 174 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 36:
;
; US-09-818-066-36
;
Query Match          59.0%; Score 36; DB 9; Length 174;
Best Local Similarity 63.6%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 LSSIFSRIGDP 12
Db      161 ISSISARTGDP 171

RESULT 37
; US-10-169-668-4
; Sequence 4, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
;   APPLICANT: BIOMERIEUX
```

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
;
; US-09-818-066-36
;
Query Match          59.0%; Score 36; DB 9; Length 174;
Best Local Similarity 63.6%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 LSSIFSRIGDP 12
Db      161 ISSISARTGDP 171

RESULT 36
; US-09-818-066-52
; Sequence 52, Application US/09818066
; Patent No. US20020032307A1
; GENERAL INFORMATION:
;   APPLICANT: Shuping Tong et al.
;   TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
;   NUMBER OF SEQUENCES: 75
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: Fish & Richardson P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: U.S.A.
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/818,066
;     FILING DATE: 27-Mar-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/683,262
;     FILING DATE: 18-JUL-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Fraser, Janis K.
;       REGISTRATION NUMBER: 31,819
;     REFERENCE/DOCKET NUMBER: 00786/287002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (617) 542-5070
;       TELEFAX: (617) 542-8906
;       TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 52:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 174 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 52:
;
; US-09-818-066-52
;
Query Match          59.0%; Score 36; DB 9; Length 174;
Best Local Similarity 63.6%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 LSSIFSRIGDP 12
Db      161 ISSISARTGDP 171

RESULT 37
; US-10-169-668-4
; Sequence 4, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
;   APPLICANT: BIOMERIEUX
```

```
/ APPLICANT: INSEEM
/ TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
/ FILE OF INVENTION: CONSTITUENTS AND USES THEREOF
/ FILE REFERENCE: IFB 99 INS HBVM
/ CURRENT APPLICATION NUMBER: US/10/169,668
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 174
/ TYPE: PRT
/ ORGANISM: mutated hepatitis B virus MHV
US-10-169-668-4

Query Match          59.0%; Score 36; DB 16; Length 174;
Best Local Similarity 63.6%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LSISFRIQDP 12
Db 161 ISSISARTGDP 171

RESULT 38
US-09-864-761-39796
/ Sequence 39796; Application US/09664761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Aemica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
```

```
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 39796
/ LENGTH: 96
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC005691.1
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 16
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 17
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 21
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 18
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 19
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 29
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 21
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 24
/ OTHER INFORMATION: EST_HUMAN HIT: AM028249.1, EVALUATE 1.00e-04
US-09-864-761-39796

Query Match          57.4%; Score 35; DB 9; Length 96;
Best Local Similarity 63.6%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LSISFRIQDP 12
Db 64 LVSDPFRVQDP 74

RESULT 39
US-10-106-698-6697
/ Sequence 6697; Application US/10106698
/ Publication No. US20030109690A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
/ FILE REFERENCE: PA005P1
/ CURRENT APPLICATION NUMBER: US/10/106,698
/ CURRENT FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26524
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: US 60/157,137
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: US 60/163,280
/ PRIOR FILING DATE: 1999-11-03
/ NUMBER OF SEQ ID NOS: 8564
/ SOFTWARE: Patentin Ver. 3.0
/ SEQ ID NO 6697
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (13)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (27)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (37)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (57)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (59)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (85)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (86)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: MISC_FEATURE
```

```

; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6697

```

```

Query Match          57.4%; Score 35; DB 15; Length 110;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 PLSIFSRIGDP 12
    | : | : | : |
DB 23 PSCITXFARTGDP 34

```

```

RESULT 40
US-10-205-979-48
; Sequence 48; Application US/10205979
; Publication No. US20030147861A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; APPLICANT: Abernethy, Nevin
; TITLE OF INVENTION: Compounds and Methods for the Modulation
; FILE REFERENCE: 11000.1063U
; CURRENT APPLICATION NUMBER: US/10/205,979
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,446
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-205-979-48

```

```

Query Match          57.4%; Score 35; DB 12; Length 173;
Best Local Similarity 54.5%; Pred. No. 94;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 PLSIFSRIGDP 11
    | | | : | : |
DB 127 PLSIFSRIGDP 137

```

Search completed: November 6, 2003, 15:18:06
 Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2003, 15:09:39 ; Search time 21 Seconds
(without alignments)
54.954 Million cell updates/sec

Title: US-09-830-981-2

Perfect score: 61

Sequence: 1 PLSIFSRIGDP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	378	2 S41869	surface antigen -
2	61	100.0	389	1 SAVLAH	large surface anti
3	61	100.0	389	2 S20749	surface antigen -
4	59	96.7	389	1 SAVLBH	large surface anti
5	59	96.7	389	1 SAVLAJ	large surface anti
6	59	96.7	389	1 SAVLAI	large surface anti
7	59	96.7	389	2 S47407	surface antigen -
8	59	96.7	389	2 S32202	large surface anti
9	54	88.5	384	2 T13474	large surface anti
10	54	88.5	384	2 T13469	large surface anti
11	54	88.5	389	2 S20745	surface antigen -
12	54	88.5	400	1 SAVLA	large surface anti
13	54	88.5	400	2 S35528	surface antigen -
14	54	88.5	445	2 S43492	surface antigen -
15	47	77.0	389	2 S67506	large surface anti
16	45	73.8	378	2 S41870	surface antigen -
17	45	73.8	389	2 S20753	surface antigen -
18	43	70.5	358	2 B81194	conserved hypotet
19	43	70.5	358	2 A81831	hypothetical prote
20	41	67.2	502	2 C87709	ubiquitome biosynt
21	40	65.6	389	1 SAVLCP	large surface anti
22	40	65.6	389	2 S41871	surface antigen -
23	39	63.9	399	2 AF2349	hypothetical prote
24	39	63.9	557	4 S42326	hypothetical large
25	38	62.3	278	2 AF2895	hypothetical prote
26	38	62.3	315	2 A86807	hypothetical prote
27	38	62.3	389	1 SAVLJ1	large surface anti
28	38	62.3	389	1 SAVLJ2	large surface anti
29	38	62.3	449	2 F86852	amino acid permeas

30	38	62.3	537	2 S67434	probable sterol O-
31	38	62.3	603	2 H69121	hypothetical prote
32	38	62.3	1786	1 H71527	probable exinucle
33	37	60.7	134	2 A82455	hypothetical prote
34	37	60.7	134	2 G82477	hypothetical prote
35	37	60.7	229	2 A97370	hypothetical prote
36	37	60.7	229	2 A12587	conserved hypotet
37	37	60.7	333	2 A90956	probable integrase
38	37	60.7	333	2 F85804	integrase for prop
39	37	60.7	422	2 T50516	retinoid x recepto
40	37	60.7	495	2 T21115	hypothetical prote
41	37	60.7	533	1 S74401	hypothetical prote
42	37	60.7	582	2 D84362	hypothetical prote
43	37	60.7	1037	2 E84723	hypothetical prote
44	36.5	59.8	335	2 G86326	protein F18014.7 l
45	36	59.0	230	2 A75260	hypothetical prote

ALIGNMENTS

RESULT 1
S41869
surface antigen - hepatitis B virus (subtype ayw, patient A) (fragment)
N/Alternate names: envelope protein, Hbs antigen
N/Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (ml
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, patient A
C/Date: 06-Jan-1995 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
R/Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.
submitted to the EMBL Data Library, January 1994
A/Description: Sequence analysis of HBV genomes isolated from patients with HBeAg chron
A/Reference number: S41869
A/Accession: S41869
A/Molecule type: DNA
A/Residues: 1-378 <LAI>
A/Cross-references: EMBL:X77309; NID:9452611; PIDN:CA54515.1; PID:9452612
A/Experimental source: subtype ayw, patient A
C/Genetics:
A/Gene: S
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: surface antigen
F/1-378/Product: surface antigen pre-S1 (large envelope protein) #status predicted <Pst>
F/1-108/Domains: pre-S1 domain #status predicted <Pst>
F/109-378/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <P
F/109-163/Domains: pre-S2 domain #status predicted <PRE2>
F/164-378/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 100.0% Score 61; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
|||||
DB 149 PLSIFSRIGDP 160

RESULT 2
SAVLAH
large surface antigen - hepatitis B virus (subtype ayw)
N/Contains: major surface antigen; middle surface antigen
C/Species: hepatitis B virus, HBV
C/Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 07-May-1999
C/Accession: A03703; J02064; P00591
R/Galibert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.
Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.
A/Reference number: A93214; MUID:81012091; PMID:399327
A/Accession: A03703
A/Molecule type: DNA
A/Residues: 1-389 <GAL>
A/Cross-references: GB:J02203

R:Norder, H.; Hammam, B.; Lee, S.D.; Bile, K.; Courouge, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993
A>Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A/Reference number: JQ2044; PMID:93329382; PMID:8336122
A/Accession: JQ2064
A/Molecule type: DNA
A/Residues: 164-389 <NOR>
A/Experimental source: Genogroup D, subtype ayw3
R:Norder, H.; Courouge, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A>Title: Molecular basis of hepatitis B virus serotype variations within the four major
A/Reference number: PQ0453; PMID:93107848; PMID:1469353
A/Accession: PQ0591
A/Molecule type: DNA
A/Residues: 264-343 <NO2>
A/Experimental source: subtype ayw3, KI1
C/Genetics:
A/Gene: pre-S1/pre-S2/S
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: glycoprotein; surface antigen
F:109-389/Product: middle surface antigen (gene S) #status predicted <MSA>
F:164-389/Product: major surface antigen (gene S) #status predicted
F:4,112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 61; DB 1; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSIFSRIGDP 12
DB 149 PLSSIFSRIGDP 160

RESULT 3

Surface antigen - hepatitis B virus (subtype ayw, patient CI)
N:Alternate names: envelope protein; HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen S (small en
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, patient CI
C/Date: 20-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
A/Accession: S20749
A/Molecule type: DNA
A/Residues: 1-389 <LAI>
A/Cross-references: EMBL:X65258; NID:G59434; PIDN:CAA46353.1; PID:G59435
A/Experimental source: subtype ayw, patient CI
A/Note: typical methionine for the beginning of pre-S2 domain at position 109 is missing
C/Genetics:
A/Gene: S
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: surface antigen
F:1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 100.0%; Score 61; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSIFSRIGDP 12
DB 149 PLSSIFSRIGDP 160

RESULT 4

SAVLBH
large surface antigen - hepatitis B virus (subtype ayw, strain PHB320)
N:Contains: major surface antigen; middle surface antigen
C/Species: hepatitis B virus, HBV

A/Note: host Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 28-Jul-2000
A/Accession: A03704; PQ0585
R:Bicho, V.; Pushko, P.; Dreilina, D.; Pumpen, P.; Gren, E.
FEBS Lett. 185, 208-212, 1985
A>Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.
A/Reference number: A05237; PMID:85204397; PMID:3996597
A/Accession: A03704
A/Molecule type: DNA
A/Residues: 1-389 <BIG>
A/Cross-references: GB:X02496; NID:962280; PIDN:CAB41701.1; PID:94704321
R:Norder, H.; Courouge, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A>Title: Molecular basis of hepatitis B virus serotype variations within the four major
A/Reference number: PQ0453; PMID:93107848; PMID:1469353
A/Accession: PQ0585
A/Molecule type: DNA
A/Residues: 264-343 <NOR>
A/Experimental source: subtype ayw2, Tav
C/Genetics:
A/Gene: pre-S1/pre-S2/S
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: glycoprotein; surface antigen
F:109-389/Product: middle surface antigen (gene S) #status predicted <MSA>
F:164-389/Product: major surface antigen (gene S) #status predicted
F:4,112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.7%; Score 59; DB 1; Length 389;
Best Local Similarity 91.7%; Pred. No. 0.0029;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSIFSRIGDP 12
DB 149 PLSSIFSRIGDP 160

RESULT 5

SAVLAI
large surface antigen - hepatitis B virus (subtype adyw)
N:Contains: major surface antigen; middle surface antigen
C/Species: hepatitis B virus, HBV
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Nov-1996
A/Accession: A93217; A03703
R:Pasek, M.; Goto, T.; Gilbert, W.; Zink, B.; Schaller, H.; Mackay, P.; Leadbetter, G.;
Nature 287, 575-579, 1979
A>Title: Hepatitis B virus genes and their expression in E. coli.
A/Reference number: A93217; PMID:8101215; PMID:399329
A/Accession: A93217
A/Molecule type: DNA
A/Residues: 1-389 <PAS>
A/Cross-references: GB:J02202
C/Genetics:
A/Gene: pre-S1/pre-S2/S
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: glycoprotein; surface antigen
F:109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <MSA>
F:164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F:4,112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.7%; Score 59; DB 1; Length 389;
Best Local Similarity 91.7%; Pred. No. 0.0029;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSIFSRIGDP 12
DB 149 PLSSIFSRIGDP 160

RESULT 6

SAVLAI
large surface antigen - hepatitis B virus (strain alpha1)
N:Contains: major surface antigen; middle surface antigen
C/Species: hepatitis B virus, HBV

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C/Accession: B34773; JQ2082
R/Tong, S.; Li, J.; Valtvicki, L.; Trepo, C.
Virology 176, 596-603, 1990
A/Title: Active hepatitis B virus replication in the presence of anti-HBe is associated
A/Reference number: A34773; MUID:9026476; PMID:2345966
A/Accession: B34773
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-389 <TON>
A/Cross-references: EMBL:M32138; NID:g329667; PIDN:AAA45502.1; PID:g329669
R/Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,
J. Gen. Virol. 74, 1341-1348, 1993
A/Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A/Reference number: JQ2044; MUID:93329382; PMID:8336122
A/Accession: JQ2082
A/Molecule type: DNA
A/Residues: 164-389 <NOR>
A/Experimental source: genogroup D, subtype ayw2, strain HBV-alpha
C/Genetics:
A/Introns: 111/3
A/pre-S1/pre-S2/S
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: glycoprotein; surface antigen (gene pre-S2/S) #status predicted <DSa>
F.109-389/Product: middle surface antigen (gene S) #status predicted <MSA>
F.164-389/Product: major surface antigen (gene S) #status predicted
F.4,112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.7%; Score 59; DB 1; Length 389;
Best Local Similarity 91.7%; Pred. No. 0.0029;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
Db 149 PLSIFSRIGDP 160

RESULT 7
S47407
surface antigen - hepatitis B virus (subtype ayw4)
N/Alternate names: envelope protein, Hbs antigen
N/Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw4
C/Date: 23-Nov-1994 #sequence_revision 12-May-1995 #text_change 26-Aug-1999
C/Accession: S47407; JQ2071
R/Plucienniczak, A.
submitted to the EMBL Data Library, August 1994
A/Description: Molecular cloning and sequencing of two complete genomes of polish isolat
A/Reference number: S47404
A/Accession: S47407
A/Molecule type: DNA
A/Residues: 1-389 <PLU>
A/Cross-references: EMBL:Z35716; NID:g527435; PIDN:CAA84788.1; PID:g527439
A/Experimental source: subtype ayw4
R/Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,
J. Gen. Virol. 74, 1341-1348, 1993
A/Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A/Reference number: JQ2044; MUID:93329382; PMID:8336122
A/Accession: JQ2071
A/Molecule type: DNA
A/Residues: 164-389 <NOR>
A/Experimental source: subtype ayw3, strain 8950/90
C/Genetics:
A/Introns: 111/3
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: surface antigen
F.1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F.1-108/Domain: pre-S1 domain #status predicted <PRE1>
F.109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F
F.109-163/Domain: pre-S2 domain #status predicted <PRE2>

F.164-389/Product: surface antigen S (small envelope protein) #status predicted <SAG>

Query Match 96.7%; Score 59; DB 2; Length 389;
Best Local Similarity 91.7%; Pred. No. 0.0029;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
Db 149 PLSIFSRIGDP 160

RESULT 8
S32202
large surface antigen - hepatitis B virus (subtype ayw, isolate patient C1005)
N/Contains: major surface antigen; middle surface antigen
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, isolate patient C1005
C/Date: 20-Feb-1995 #sequence_revision 06-Dec-1996 #text_change 06-Dec-1996
R/Pretzler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Gero, W.; Rasenack, J.
submitted to the EMBL Data Library, March 1993
A/Description: Identification and sequence analysis of hepatitis B virus DNA in immunolc
A/Reference number: S32202
A/Accession: S32202
A/Molecule type: DNA
A/Residues: 1-389 <PRE>
A/Cross-references: EMBL:X72702
A/Experimental source: subtype ayw, isolate patient C1005
C/Genetics:
A/Introns: 111/3
A/pre-S1/pre-S2/S
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: surface antigen
F.1-389/Product: large surface antigen (gene pre-S1/pre-S2/S) #status predicted <DSL>
F.109-389/Product: middle surface antigen (gene S) #status predicted <MSA>
F.164-389/Product: major surface antigen (gene S) #status predicted <MSA>

Query Match 96.7%; Score 59; DB 2; Length 389;
Best Local Similarity 91.7%; Pred. No. 0.0029;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
Db 149 PLSIFSRIGDP 160

RESULT 9
T13474
large surface antigen - hepatitis B virus (isolate 29Y11HC)
N/Alternate names: envelope protein, Hbs antigen
N/Contains: major surface antigen; middle surface antigen
C/Species: hepatitis B virus, HBV
A/Variety: isolate 29Y11HC
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C/Accession: T13474
R/Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishi, S.
Arch. Virol. 143, 2313-2326, 1998
A/Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcino
A/Reference number: Z17684; MUID:99129050; PMID:9930189
A/Accession: T13474
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-382 <TAK>
A/Cross-references: EMBL:AB014388; NID:g3582381; PIDN:BA32936.1; PID:g3582384
A/Experimental source: Japanese patient with hepatocellular carcinoma isolate 29Y11HC
C/Genetics:
A/Introns: 123/2
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: glycoprotein; surface antigen

Query Match 88.5%; Score 54; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 0.025;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSSIFSRIGDP 12
|:|||||
Db 142 PLSSIFSRIGDP 153

RESULT 10

113469
large surface antigen - hepatitis B virus (isolate 09D09HCC)
N:Alternate names: envelope protein
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate 09D09HCC
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
A:Accession: 113469
R:Nakhaishi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishiro, S.
Arch. Virol. 143, 2313-2326, 1998
A:Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcin
A:Reference number: 217684; PMID:99129050; PMID:9910189
A:Accession: 113469
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-384 <TRK>
A:Cross-references: EMBL:AB014368; NID:G3551304; PIDN:BA432864.1; PID:G3551308
A:Experimental source: Japanese patient with hepatocellular carcinoma isolate 09D09HCC
C:Genetics:
A:Gene: S
A:Introns: 123/2
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen

Query Match 88.5%; Score 54; DB 2; Length 384;
Best Local Similarity 83.3%; Pred. No. 0.025;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSSIFSRIGDP 12
|:|||||
Db 144 PLSSIFSRIGDP 155

RESULT 11

S20745
surface antigen - hepatitis B virus (subtype ayw, patient C)
N:Alternate names: HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient C
C>Date: 20-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
C:Accession: S20745
R:Iral, M.B.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.
Submitted to the EMBL Data Library, March 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati
A:Reference number: S20745
A:Accession: S20745
A:Molecule type: DNA
A:Residues: 1-389 <RAI>
A:Cross-references: EMBL:X65257; NID:G59429; PIDN:CA46349.1; PID:G59430
A:Experimental source: subtype ayw, patient C
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen
F:1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-108/Domains: pre-S1 domain #status predicted <PRE1>
F:109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <P
F:109-163/Domains: pre-S2 domain #status predicted <PRE2>
F:164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 88.5%; Score 54; DB 2; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12

Db 150 LSSIFSRIGDP 160
|||||

RESULT 12

SAVLA
large surface antigen - hepatitis B virus (subtype adr)
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 07-May-1999
C:Accession: A03705; S04568; J02107; P00608
R:Ono, Y.; Ono, H.; Sasada, R.; Igatah, K.; Sugino, Y.; Nishioka, K.
Nucleic Acids Res. 11, 1747-1757, 1983
A:Title: The complete nucleotide sequences of the cloned hepatitis B virus DNA; subtype
A:Reference number: A93460; PMID:83168919; PMID:6300776
A:Accession: A03705
A:Molecule type: DNA
A:Residues: 1-400 <ONO>
A:Cross-references: GB:V00867
R:Rho, H.M.; Kim, K.; Hyun, S.W.; Kim, Y.S.
Nucleic Acids Res. 17, 2124, 1989
A:Title: The nucleotide sequence and reading frames of a mutant hepatitis B virus subtyp
A:Reference number: S04568; PMID:89183619; PMID:2928116
A:Accession: S04569
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-50, 'R', 52-66, 'YP', 69-129, 'V', 131-142, 'P', 144-164, 'S', 166-176, 'S', 178-338, '
A:Cross-references: EMBL:X14193
R:Norde, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus, J.
J. Gen. Virol. 74, 1341-1348, 1993
A:Title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: J02044; PMID:93329382; PMID:8336122
A:Accession: J02107
A:Molecule type: DNA
A:Residues: 175-400 <NOR>
A:Experimental source: genogroup C, subtype adr, strain pBRHBadr4
R:Norde, H.; Courouce, A.M.; Magnus, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A:Title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: P00453; PMID:93107848; PMID:1469553
A:Accession: P00608
A:Molecule type: DNA
A:Residues: 275-354 <NO2>
A:Experimental source: subtype adr, Bau

C:Genetics:
A:Gene: pre-S1/pre-S2/S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F:120-400/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F:175-400/Product: major surface antigen (gene S) #status predicted <WSA>
F:15,123,177/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 88.5%; Score 54; DB 1; Length 400;
Best Local Similarity 83.3%; Pred. No. 0.026;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSSIFSRIGDP 12
|:|||||
Db 160 PLSSIFSRIGDP 171

RESULT 13

S35528
surface antigen - hepatitis B virus (subtype adr)
N:Alternate names: envelope protein; HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype adr
C>Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S35528
R:Mukhaide, M.; Kumazawa, T.; Hoshi, A.; Kawaguchi, R.; Hiki, J.
Nucleic Acids Res. 20, 6105, 1992
A:Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) and

A:Reference number: S35527; MUID:93096607; PMID:1461746
A:Accession: S35528
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-400 <MUK>
A:Cross-References: EMBL:D12980; NID:g221500; PIDN:BAA03359.1; PID:g221502
A:Experimental source: subtype adr
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
C:Genetics:
A:Gene: S
A:Introns: 165/2
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen
F:1-400/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-119/Domain: pre-S1 domain #status predicted <PRE1>
F:120-400/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F>
F:120-174/Domain: pre-S2 domain #status predicted <PRE2>
F:175-400/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 88.5%; Score 54; DB 2; Length 400;
Best Local Similarity 83.3%; Pred. No. 0.026;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFRTGDP 12
DB 160 PLSISFRTGDP 171

RESULT 14
S34392
surface antigen - hepatitis B virus (subtype adr)
N:Alternate names: HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype adr
C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
C:Accession: S43492; PNO601; PNO602
R:Longarcvic, I.F.; Zentgraf, H.; Schroeder, C.H.
Nucleic Acids Res. 18, 4940, 1990
A>Title: Sequence of a replication competent hepatitis B virus genome with a preX open r
A:Reference number: S12598; MUID:90370503; PMID:2395664
A:Accession: S43492
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-445 <LON>
A:Cross-References: EMBL:X52939; NID:g457780; PIDN:CAA37114.1; PID:g457783
A:Experimental source: subtype adr
R:Mims, L.T.; Solomon, L.R.; Ebert, J.W.; Fields, H.
Biochem. Biophys. Res. Commun. 195, 186-191, 1993
A>Title: Unique PreS sequence in a gibbon-derived hepatitis B virus variant.
A:Reference number: PNO601; MUID:93371402; PMID:8363598
A:Accession: PNO601
A:Molecule type: protein
A:Residues: 57-95 <MIM>
A:Accession: PNO602
A:Molecule type: protein
A:Residues: 165-196 <MT2>
C:Genetics:
A:Gene: S
A:Introns: 210/3
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen
F:1-445/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-164/Domain: pre-S1 domain #status predicted <PRE1>
F:165-445/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F>
F:165-219/Domain: pre-S2 domain #status predicted <PRE2>
F:220-445/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 88.5%; Score 54; DB 2; Length 445;
Best Local Similarity 83.3%; Pred. No. 0.029;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSISFRTGDP 12

DB 205 PLSISFRTGDP 216

RESULT 15
S67506
large surface antigen - hepatitis B virus (subtype ayw3, isolate Hope CH1357)
N:Alternate names: envelope protein, HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw3, isolate Hope CH1357
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 26-Aug-1999
C:Accession: S67506
R:Norder, H.; Ebert, J.W.; Fields, H.A.; Mushawar, I.K.; Magnus, L.O.
Virology 218, 214-223, 1996
A>Title: Complete sequencing of a gibbon hepatitis B virus genome reveals a unique genot
A:Reference number: S67503; MUID:96207410; PMID:8615024
A:Accession: S67506
A:Molecule type: DNA
A:Residues: 1-389 <NOR>
A:Cross-References: EMBL:U46935; NID:g1814218; PIDN:AAB41952.1; PID:g1814222
A:Experimental source: subtype ayw3, isolate Hope CH1357
C:Genetics:
A:Gene: pre-S1/pre-S2/S
A:Introns: 112/2
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein, surface antigen
F:1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-108/Domain: pre-S1-specific domain #status predicted <PRE1>
F:109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F>
F:109-163/Domain: pre-S2-specific domain #status predicted <PRE2>
F:164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>
F:4,112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 77.0%; Score 47; DB 2; Length 389;
Best Local Similarity 81.8%; Pred. No. 0.54;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSISFRTGDP 12
DB 150 PLSISFRTGDP 160

RESULT 16
S41870
surface antigen - hepatitis B virus (subtype ayw, patient M) (fragment)
N:Alternate names: envelope protein, HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient M
C:Date: 06-Jan-1995 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
C:Accession: S41870
R:Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.
submitted to the EMBL Data Library, January 1994
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg chroni
A:Reference number: S41869
A:Accession: S41870
A:Molecule type: DNA
A:Residues: 1-378 <LAI>
A:Cross-References: EMBL:X77308; NID:g452613; PIDN:CAA54514.1; PID:g452614
A:Experimental source: subtype ayw, patient M
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen
F:1-378/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-108/Domain: pre-S1 domain #status predicted <PRE1>
F:109-378/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F>
F:109-163/Domain: pre-S2 domain #status predicted <PRE2>
F:164-378/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 73.8%; Score 45; DB 2; Length 378;
Best Local Similarity 75.0%; Pred. No. 1.3;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PLSISFRIGDP 12
|||||:|||||
Db 149 PLSISARTGDP 160

RESULT 17

S20753
surface antigen - hepatitis B virus (subtype ayw, patient E)
N:Alternate names: envelope protein; HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient E
C:Date: 20-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
C:Accession: S20753
R:Jai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negativ
A:Reference number: S20745
A:Accession: S20753
A:Molecule type: DNA
A:Residues: 1-389 <LAI>
A:Cross-references: EMBL:X65259; NID:g59439; PIDN:CAA46357.1; PID:g59440
A:Experimental source: subtype ayw, patient E
C:Genetics:

A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen
F:1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-108/Domain: pre-S1 domain #status predicted <PRE1>
F:109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F
F:109-163/Domain: pre-S2 domain #status predicted <PRE2>
F:164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 73.8%; Score 45; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PLSISFRIGDP 12
|||||:|||||
Db 149 PLSISARTGDP 160

RESULT 18

B81194
conserved hypothetical protein NMB0471 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: B81194
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 267, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:2015755; PMID:10710307
A:Accession: B81194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <TEY>
A:Cross-references: GB:AE002404; GB:AE002098; NID:g7225697; PIDN:AAF40908.1; PID:g722569
A:Experimental source: serogroup B, strain MC58
C:Genetics:

A:Gene: NMB0471
Query Match 70.5%; Score 43; DB 2; Length 358;
Best Local Similarity 58.3%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 12
|||:|:|:|
Db 121 PLGPVFRIGDP 132

RESULT 19

A81831
hypothetical protein NMA2014 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81831
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: A81831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <PAR>
A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85233.1; PID:g738064
A:Experimental source: serogroup A, strain Z2491
C:Genetics:

A:Gene: NMA2014
Query Match 70.5%; Score 43; DB 2; Length 358;
Best Local Similarity 58.3%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 12
|||:|:|:|
Db 121 PLGPVFRIGDP 132

RESULT 20

C87709
ubiquitinone biosynthesis protein Aarf, probable [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: C87709
R:Meram, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; Debroy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <STO>
A:Cross-references: GB:AE005673; NID:g13425475; PIDN:AAK25671.1; GSPDB:GN00148
A:Genetics:

A:Gene: CC3709
C:Superfamily: Synchocystis ABC transporter slr1919
Query Match 67.2%; Score 41; DB 2; Length 502;
Best Local Similarity 58.3%; Pred. No. 9.9;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 21

SAV1CP
large surface antigen - hepatitis B virus
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jun-2000
C:Accession: C28885; J02123
R:Yaudin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.
J. Gen. Virol. 69, 1383-1389, 1988
A:Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated
A:Reference number: A97796; MUID:88258473; PMID:2838576
A:Accession: C28885

A:Molecule type: DNA
A:Residues: 1-389 <VAV>
A:Cross-references: GB:D00220; NID:9221505; PIDN:BA00159.1; PID:9221508
A:Experimental source: strain LSH, chimpanzee
A:Note: the authors translated the codon GAG for residue 327 as Gln
R:Order: H.; Hammes, B.; Lee, S.D.; Bille, K.; Courouce, A.M.; Muehalwar, I.K.; Magnus, J. Gen. Virol. 74, 1341-1348, 1993
A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A:Reference number: JQ2044; MUID:93329382; PMID:8336122
A:Accession: JQ2123
A:Molecule type: DNA
A:Residues: 164-389 <NOR>
A:Experimental source: subtype adw2, strain adwLSH
C:Genetics:
A:Gene: pre-S1/pre-S2/S; S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F:109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F:164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F:4,112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.6%; Score 40; DB 1; Length 389;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
:|||||
Db 150 ISSVFTTQDP 160

RESULT 22
S41871
surface antigen - hepatitis B virus (subtype ayw, patient P)
N:Alternate names: envelope protein, HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient P
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S41871
R:Lat, M.E.; Marzoteni, A.P.; Balestrieri, A.
Submitted to the EMBL Data Library, January 1994
A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg chroni
A:Reference number: S41869
A:Accession: S41871
A:Molecule type: DNA
A:Residues: 1-389 <LAT>
A:Cross-references: EMBL:X77310; NID:9452615; PIDN:CAA54516.1; PID:9452616
A:Experimental source: subtype ayw, patient P
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen
F:1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-108/Domain: pre-S1 domain #status predicted <PRE1>
F:109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <H
F:164-389/Domain: pre-S2 domain #status predicted <PRE2>
F:164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 65.6%; Score 40; DB 2; Length 389;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
:|||||
Db 150 ISSVFTTQDP 160

RESULT 23
AF2349
hypothetical protein al14349 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AF2349
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritschi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 6, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2349
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <KUR>
A:Cross-references: GB:BA00019; PIDN:BA076048.1; PID:917133485; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: al14349

Query Match 63.9%; Score 39; DB 2; Length 399;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
:|||||
Db 351 PMSRFTTQDP 362

RESULT 24
S42226
hypothetical large surface antigen/mevalonate kinase (EC 2.7.1.36) mutant fusion protein
C:Species: hepatitis B virus, HBV
C:Date: 13-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 20-Oct-2000
C:Accession: S42226
R:Graef, E.; Caselmann, W.H.; Wells, J.; Koshy, R.
Oncogene 9, 81-87, 1994
A:Title: Insertional activation of mevalonate kinase by hepatitis B virus DNA in a human
A:Reference number: S42226; MUID:94134441; PMID:8302606
A:Accession: S42226
A:Molecule type: mRNA
A:Residues: 1-557 <GRA>
A:Cross-references: EMBL:X75311; NID:9450345; PIDN:CAA53059.1; PID:9450346
C:Keywords: phosphotransferase
F:1-157/Region: hepatitis B virus large surface antigen (fragment)
F:162-557/Region: human mevalonate kinase (fragment)

Query Match 63.9%; Score 39; DB 4; Length 557;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
:|||||
Db 42 ISSVFTTQDP 52

RESULT 25
AF2895
hypothetical protein Atu2599 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AF2895
R:Wood, D.W.; Setudal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
Beer, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-278 <KUR>
A:Cross-references: GB:AE00688; PIDN:AAL43580.1; PID:917741096; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2599

A:Map position: circular chromosome

Query Match 62.3%; Score 38; DB 2; Length 278;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 11
|||:||||
DB 211 PLUKFSRFGD 221

RESULT 26

A:86807

hypothetical protein yoiB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C/Accession: A86807

R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Saastrosowigmo, R.I.; Imai, M.; Miyakawa, Y.; Ehrlich

Genome Res. 11, 731-753, 2001

A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

F/4,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

A/Accession: A86807

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-315 <STO>

A/Cross-references: GB:AE005176; PID:g12724449; PIDN:AAK0555.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: yoiB

Query Match 62.3%; Score 38; DB 2; Length 315;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRIG 10
|||||:|
DB 21 PLSISYNOIG 30

RESULT 27

SAVLJ1

large surface antigen - hepatitis B virus (subtype adw, strain Japan/pJDM233)

N:Contains: major surface antigen; middle surface antigen

C:Species: hepatitis B virus, HBV

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 14-Nov-1997

C/Accession: G28925

R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Saastrosowigmo, R.I.; Imai, M.; Miyakawa, Y.; V

J. Gen. Virol. 69, 2575-2583, 1988

A>Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf

A/Reference number: JS0253; MUID:89010694; PMID:3171552

A/Accession: G28925

A/Molecule type: DNA

A/Residues: 1-389 <OKA>

A/Cross-references: GB:D00329; NID:g221497

C:Genetics:

A:Gene: pre-S1/pre-S2/S

C:Superfamily: hepatitis B virus surface antigen

C/Keywords: glycoprotein; surface antigen (gene pre-S2/S) #status predicted <DSA>

F/109-389/Product: middle surface antigen (gene S) #status predicted <MSA>

F/175-389/Product: major surface antigen (gene S) #status predicted <MSA>

F/4,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.3%; Score 38; DB 1; Length 389;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSISFRIGDP 12
|||:|:|
DB 150 ISSILSKTGP 160

RESULT 28

SAVLJ2

large surface antigen - hepatitis B virus (subtype adw, strain Okinawa/pODW282)

N:Contains: major surface antigen; middle surface antigen

C:Species: hepatitis B virus, HBV

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 14-Nov-1997

C/Accession: H28925

R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Saastrosowigmo, R.I.; Imai, M.; Miyakawa, Y.; I

J. Gen. Virol. 69, 2575-2583, 1988

A>Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf

A/Reference number: JS0253; MUID:89010694; PMID:3171552

A/Accession: H28925

A/Molecule type: DNA

A/Residues: 1-389 <OKA>

A/Cross-references: GB:D00330; NID:g221498

C:Genetics:

A:Gene: pre-S1/pre-S2/S

C:Superfamily: hepatitis B virus surface antigen

C/Keywords: glycoprotein; surface antigen (gene pre-S2/S) #status predicted <DSA>

F/109-389/Product: middle surface antigen (gene S) #status predicted <MSA>

F/164-389/Product: major surface antigen (gene S) #status predicted <MSA>

F/4,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.3%; Score 38; DB 1; Length 389;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSISFRIGDP 12
|||:|:|
DB 150 ISSILSKTGP 160

RESULT 29

F86852

amino acid permease ysjA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C/Accession: F86852

R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Saastrosowigmo, R.I.; Imai, M.; Miyakawa, Y.; Ehrlich

Genome Res. 11, 731-753, 2001

A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A/Reference number: A86825; MUID:21235186; PMID:11337471

A/Accession: F86852

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-449 <STO>

A/Cross-references: GB:AE005176; PID:g12724850; PIDN:AAK05920.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: ysjA

C:Superfamily: arginine permease

Query Match 62.3%; Score 38; DB 2; Length 449;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 12
|||:|:|
DB 276 PFATIFARVGP 287

RESULT 30

S67434

probable sterol O-acetyltransferase (EC 2.3.1.26) SPAC13G7.05 [similarity] - fission yeast

C:Species: Schizosaccharomyces pombe

C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 08-Sep-2000

C/Accession: S67434; J17655

R:Connor, R.; Churcher, C.M.

submitted to the EMBL Data Library, February 1996

A/Reference number: S67430

A/Accession: S67434

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-537 <CON>

A/Cross-references: EMBL:Z69729; NID:g1204167; PIDN:CAA93593.1; PID:g223696; PID:g120417

Db 74 LSSIFSGWGP 84

RESULT 35

A97370
hypothetical protein AGR_C.144 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C/Accession: A97370
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Marwitz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: A97370
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-229 <KUR>
A/Cross-references: GB:AE007869; PIDN:AAK85914.1; PID:G15154963; GSPDB:GN00169
C/Genetics:
A/Gene: AGR_C.144
A/Map position: circular chromosome

Query Match 60.7%; Score 37; DB 2; Length 229;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
|:::|||||
Db 141 PCATLSARIGDP 152

RESULT 36

A12587
conserved hypothetical protein Atu0094 [imported] - Agrobacterium tumefaciens (strain C5
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C/Accession: A12587
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: A12587
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-229 <KUR>
A/Cross-references: GB:AE008688; PIDN:AAI41119.1; PID:G17738412; GSPDB:GN00186
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: Atu0094
A/Map position: circular chromosome

Query Match 60.7%; Score 37; DB 2; Length 229;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
|:::|||||
Db 141 PCATLSARIGDP 152

RESULT 37

A90956
probable integrase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C/Accession: A90956
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: A90956
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333 <NAV>
A/Cross-references: GB:BA000007; PIDN:BA936040.1; PID:G13362085; GSPDB:GN00154
C/Genetics:
A/Gene: Ece2617
C/Superfamily: phage P22 integrase

Query Match 60.7%; Score 37; DB 2; Length 333;
Best Local Similarity 63.6%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
|:::|||||
Db 84 LEAICSRIGDP 94

RESULT 38

F85804
integrase for prophage CP-933r [imported] - Escherichia coli (strain O157:H7, substrain
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: F85804
R/Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayne-
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimlantia, E.; Potamoustis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: F85804
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-333 <STO>
A/Cross-references: GB:AE005174; NID:G12515975; PIDN:AA656898.1; GSPDB:GN00145; UMGF:225
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: intT
C/Superfamily: phage P22 integrase

Query Match 60.7%; Score 37; DB 2; Length 333;
Best Local Similarity 63.6%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
|:::|||||
Db 84 LEAICSRIGDP 94

RESULT 39

I50516
retinoid X receptor delta - zebra fish
C/Species: Brachydanio rerio (zebra fish)
C/Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 02-Aug-2002
C/Accession: I50516
R/Jones, B.B.; Ohno, C.K.; Allenby, G.; Boffa, M.B.; Levin, A.A.; Grippo, J.F.; Petkovic
Mol. Cell. Biol. 15, 5226-5234, 1995
A/Title: New retinoid X receptor subtypes in zebra fish (Danio rerio) differentially mod
A/Reference number: A57301; MUID:96009547; PMID:7565671
A/Accession: I50516
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-422 <JON>
A/Cross-references: EMBL:U29941; NID:G1046296; PIDN:AAC59721.1; PID:G1046297
C/Genetics:
A/Gene: RXR
C/Superfamily: retinoic acid receptor alpha; erba transforming protein homology
C/Keywords: zinc finger
F/88-341/Domain: erba transforming protein homology <ERBA>

Query Match 60.7%; Score 37; DB 2; Length 422;
 Best Local Similarity 58.3%; Pred. No. 47;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
 |||::|||
 Db 21 PLSAVSSSIGSP 32

RESULT 40

T21115
 hypothetical protein F19C6.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T21115
 R:Haris, B.
 submitted to the EMBL Data Library, January 1995
 A:Reference number: Z19376
 A:Accession: T21115
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-495 <MIT>
 A:Cross-references: EMBL:Z48006; PIDN:CA88050.1; GSPDB:GN00028; CESP:F19C6.2
 A:Experimental source: clone F19C6
 C:Genetics:
 A:Gene: CESP:F19C6.2
 A:Map position: X
 A:Introns: 44/1; 117/3; 153/3; 213/3; 238/3; 334/1; 387/2; 417/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein F19C6.2

Query Match 60.7%; Score 37; DB 2; Length 495;
 Best Local Similarity 45.5%; Pred. No. 56;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGD 11
 |::|::|
 Db 278 PVSGLFOKVGD 288

Search completed: November 6, 2003, 15:13:16
 UOD time : 23 secs

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FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 75 75 O -> E (IN STRAIN LATVIA).
 FT VARIANT 147 147 A -> S (IN STRAIN LATVIA).
 FT VARIANT 150 150 L -> I (IN STRAIN LATVIA).
 FT VARIANT 288 290 MTT -> TTP (IN STRAIN LATVIA).
 SQ SEQUENCE 389 AA; 42766 MW; 6DC9E82DA694F63 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 389;
 Best Local Similarity 100.0%; Pred. No. 0.00054;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 12
 DB 149 PLSISFRIGDP 160

RESULT 2

IDS_VMSA_HPBVA STANDARD; PRT; 389 AA.

AC P24025;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DE Major surface antigen precursor.
 GN S.
 OS Hepatitis B virus (strain alpha1).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10411;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90266476; PubMed=2345966;
 RA Tong S., Li J., Vitvitski L., Trepo C.;
 RT "Active hepatitis B virus replication in the presence of anti-HBe is
 associated with viral variants containing an inactive pre-C region.";
 RL Virology 176:596-603(1990).

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CC EMBL_M32138; AAA45502.1; -.
 DR PIR; B34773; SAVLAJ.
 DR InterPro; IPR000349; Hepvir_surfAg.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 KM PROPRP 1 163
 FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 389 AA; 42733 MW; B06D0D42B23B5 CRC64;

Query Match 96.7%; Score 59; DB 1; Length 389;
 Best Local Similarity 91.7%; Pred. No. 0.0013;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 12
 DB 149 PLSISFRIGDP 160

RESULT 3

IDS_VMSA_HPBVA STANDARD; PRT; 389 AA.

AC P03139;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-1989 (Rel. 12, Last annotation update)
 DE Major surface antigen precursor.

GN S.
 OS Hepatitis B virus (subtype adyw).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10419;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81012115; PubMed=399329;
 RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., Mackay P.,
 RA Leadbetter G., Murray K.;
 RT "Hepatitis B virus genes and their expression in E. coli.";
 RL Nature 282:575-579(1979).

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CC EMBL_J02202; AAA45487.1; ALT_INIT.
 DR PIR; A93217; SAVLAJ.
 DR InterPro; IPR000349; Hepvir_surfAg.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 KM PROPRP 1 163
 FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 389 AA; 42801 MW; 1063FE8B4679A69 CRC64;

Query Match 96.7%; Score 59; DB 1; Length 389;
 Best Local Similarity 91.7%; Pred. No. 0.0013;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 12
 DB 149 PLSISFRIGDP 160

RESULT 4

IDS_VMSA_HPBVA STANDARD; PRT; 400 AA.

AC P03140;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Major surface antigen precursor.
 GN S.
 OS Hepatitis B virus (subtype adr).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=106820;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83168919; PubMed=6300776;
 RA Ono Y., Ono H., Sasada R., Igataashi K., Sugino Y., Nishio K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 DNA: subtype adr and adr.";
 RL Nucleic Acids Res. 11:1747-1757(1983).

RN [2]
 RP SEQUENCE OF 176-350 FROM N.A.
 RX MEDLINE=85107103; PubMed=3968537;
 RA Takeshima H., Inokoshi J., Namiki M., Shimada J., Omura S.;
 RT "Structural analysis of the gene coding for hepatitis B virus surface
 antigen and its product.";
 RL J. Gen. Virol. 66:195-200(1985).

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DR EMBL; V00867; CAA24234.1; ALT_INIT.
DR PIR; A03705; SAVLA.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.

KW Antigen.
FT PROPEP 1 174
FT CHAIN 175 400
FT CARBOHYD 15 15
FT CARBOHYD 123 123
FT CARBOHYD 177 177
FT CARBOHYD 320 320
SQ SEQUENCE 400 AA; 43685 MW; 16DB0B15C6CB697A CRC64;

Query Match
Best Local Similarity 88.5%; Score 54; DB 1; Length 400;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSSISFRTGDP 12
Db 160 PSSISFRTGDP 171

RESULT 5
VMSA_HPBV4 STANDARD; PRT; 400 AA.

ID P12934; 067860;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface antigen precursor.

OS Hepatitis B virus (subtype adr).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;

RP SEQUENCE FROM N.A.
RA MEDLINE=83246570; PubMed=6306594;
RA Fujiyama A., Miyahara A., Nozaki C., Yoneyama T., Ohomo N.,
RA Matsubara K.,
RT Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr."
RL Nucleic Acids Res. 11:4601-4610(1983).

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CC EMBL; X01587; CAA25747.1; ALT_INIT.
DR EMBL; X01587; CAA25743.1; ALT_INIT.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.

KW Antigen.
FT PROPEP 1 174
FT CHAIN 175 400
FT CARBOHYD 15 15
FT CARBOHYD 123 123
FT CARBOHYD 177 177
FT CARBOHYD 320 320
SQ SEQUENCE 400 AA; 43542 MW; 01053BBBD24053F9 CRC64;

Query Match
Best Local Similarity 75.4%; Score 46; DB 1; Length 400;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSSISFRTGDP 12
Db 160 PSSISFRTGDP 171

RESULT 6
VMSA_HPBVP STANDARD; PRT; 400 AA.

ID Q02317;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen precursor.

OS Hepatitis B virus (subtype adr / strain Philippines/GFDM294).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31514;

RP SEQUENCE FROM N.A.
RA Estacio R.C., Chavez C.C., Okamoto H., Lingao A.L., Reyes M.T.,
RA Domingo E., Mayumi M.,
RT "Nucleotide sequence of a hepatitis B virus genome of subtype adr
RT isolated from a Filipino: comparison with the reported three genomes
RT of the same subtype."
RL J. Gastroenterol. Hepatol. 3:215-222(1988).

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CC EMBL; M57663; AAA69680.1;
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.

KW Antigen.
FT PROPEP 1 174
FT CHAIN 175 400
FT CARBOHYD 15 15
FT CARBOHYD 123 123
FT CARBOHYD 177 177
FT CARBOHYD 320 320
SQ SEQUENCE 400 AA; 43740 MW; 7EBD53A004136BD2 CRC64;

Query Match
Best Local Similarity 72.1%; Score 44; DB 1; Length 400;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PSSISFRTGDP 12
Db 161 PSSISFRTGDP 171

RESULT 7

ID BD02_HUMAN STANDARD; PRT; 64 AA.

AC 015263;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Beta-defensin 2 precursor (hbd-2) (Skin-antimicrobial peptide 1)
DE (SAP1).
GN DEF84 OR DEF82 OR DEF8102.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN 11)
RP SEQUENCE FROM N.A.
RT TISSUE=skin;

RX MEDLINE=97345625; PubMed=9202117;
 RA Harder J., Bartels J.H., Christophers E., Schroeder J.-M.;
 RT "A peptide antibiotic from human skin.";
 RL Nature 387:861-861(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99051334; PubMed=9831658;
 RA Liu L., Wang L., Jia H.P., Zhao C., Heng H.H.Q., Schutte B.C.,
 RA McCray P.B. Jr., Ganz T.;
 RT "Structure and mapping of the human beta-defensin HBD-2 gene and its
 expression at sites of inflammation.";
 RL Gene 222:237-244(1998).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20072673; PubMed=10603376;
 RA Diamond G., Kaiser V., Rhodes J., Russell J.P., Bevins C.L.;
 RT "Transcriptional regulation of beta-defensin gene expression in
 tracheal epithelial cells.";
 RL Infect. Immun. 68:113-119(2000).
 [4]
 RP SEQUENCE FROM N.A.
 RA Harder J., Schroeder J.M.;
 RT "Transcriptional regulation of the human beta-defensin-2 (HBD-2).";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SYNTHESIS OF 24-64.
 RX MEDLINE=2007551; PubMed=12010514;
 RA Kluver E., Schulz A., Forssmann W.-G., Adernann K.;
 RT "Chemical synthesis of beta-defensins and LEAP-1/hepcidin.";
 RL J. Pept. Res. 59:241-248(2002).
 [6]
 RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
 RX MEDLINE=20490730; PubMed=10906336;
 RA Hoover D.M., Rajashankar K.R., Blumenthal R., Puri A., Oppenheim J.J.,
 RA Chertov O., Lubkowski J.;
 RT "The structure of human beta-defensin-2 shows evidence of higher
 order oligomerization.";
 RL J. Biol. Chem. 275:32911-32918(2000).
 [7]
 RP STRUCTURE BY NMR OF 28-64.
 RX MEDLINE=21571984; PubMed=11714914;
 RA Bauer F., Schweimer K., Kluver E., Conejo-Garcia J.R.,
 RA Forssmann W.-G., Rosch P., Adernann K., Sticht H.;
 RT "Structure determination of human and murine beta-defensins reveals
 structural conservation in the absence of significant sequence
 similarity.";
 RL Protein Sci. 10:2470-2479(2001).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE SKIN AND RESPIRATORY TRACT.
 CC -1- INDUCTION: By inflammation.
 CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
 SUBFAMILY.
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 CC EMBL: Z71389; CAA95992.1; -;
 CC EMBL: AF040153; AAC3549.1; -;
 CC EMBL: AF071216; AAC69554.1; -;
 CC EMBL: AJ000152; CAB65126.1; -;
 CC PDB: 1PD3; 01-NOV-00.
 CC PDB: 1PD4; 01-NOV-00.
 CC PDB: 1E40; 26-NOV-01.
 CC PDB: 1F00; 31-DEC-02.
 CC Genew; HGNC:2767; DEFB4.
 CC MIM; 602215; -.

DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR GO; GO:000613; P:response to pest/pathogen/parasite; TAS.
 DR InterPro; IPR001855; Defensin_beta.
 DR InterPro; IPR006080; Defensin_mammal.
 DR Pfam; PF00711; Defensin_beta; 1.
 DR SMART; SM00048; DEFSN; 1.
 KM Antibiotic; Signal; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 64
 FT DISULFID 31 60
 FT DISULFID 38 53
 FT DISULFID 43 61
 FT STRAND 26 26
 FT HELIX 28 33
 FT TURN 34 35
 FT STRAND 37 39
 FT TURN 45 46
 FT STRAND 48 52
 FT TURN 56 57
 FT STRAND 59 62
 SQ SEQUENCE 64 AA; 7038 MW; 05D6454CE7ACD10E CRC64;
 Query Match 65.6%; Score 40; DB 1; Length 64;
 Best Local Similarity 58.3%; Pred. No. 0.82;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 PLSSIFSRIGDP 12
 Db 17 PLFGVFGIGDP 28
 RESULT 8
 VMSA_HPBVL STANDARD; PRT; 389 AA.
 ID VMSA_HPBVL
 AC P12911;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Major surface antigen precursor.
 GN S.
 OS Hepatitis B virus (strain 1ah / chimpanzee isolate).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_Taxid=10414;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88258473; PubMed=2838576;
 RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
 RA Harrison T.J.;
 RT "The complete nucleotide sequence of the genome of a hepatitis B
 virus isolated from a naturally infected chimpanzee.";
 RL J. Gen. Virol. 69:1383-1389(1988).
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 CC
 CC EMBL: D00220; BAA00159.1; -;
 DR PIR; C28885; SAVLCP.
 DR InterPro; IPR000349; Hepvir_surfAg.
 DR Pfam; PF00695; VMSA; 1.
 KM Antigen.
 FT PROPEP 1 163
 FT CHAIN 164 389
 FT CARBOHYD 4 4
 FT CARBOHYD 112 112
 FT CARBOHYD 166 166
 FT CARBOHYD 309 309
 MAJOR SURFACE ANTIGEN.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 389 AA; 42539 MW; 87DIP93382A10DBD CRC64;
[1]
Query Match 65.6%; Score 40; DB 1; Length 389;
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LSSIFSRIGDP 12
:|||||:
Db 150 ISSIFSTTGD 160

RESULT 9
VMSA_HPBVO STANDARD; PRT; 389 AA.
AC P17398;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain Japan/pJDM233).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10413;
RN SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Teuda F., Sakugawa H., Saetiroewignjo R.I., Imai M.,
Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
CC EMBL; D00329; -; NOT_ANNOTATED_CDS.
DR PIR; G28925; SAVLJ1.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 163
FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42603 MW; 72F8D481924DC104 CRC64;

Query Match 62.3%; Score 38; DB 1; Length 389;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LSSIFSRIGDP 12
:|||||:
Db 150 ISSIFSKTGD 160

RESULT 10
VMSA_HPBVO STANDARD; PRT; 389 AA.
AC P17399;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain Okinawa/PODW282).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10415;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Teuda F., Sakugawa H., Saetiroewignjo R.I., Imai M.,
Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
CC EMBL; D00330; -; NOT_ANNOTATED_CDS.
DR PIR; H28925; SAVLJ2.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 163
FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42408 MW; CECACDDA3D84A10 CRC64;

Query Match 62.3%; Score 38; DB 1; Length 389;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LSSIFSRIGDP 12
:|||||:
Db 150 ISSIFSKTGD 160

RESULT 11
AREH_SCHPO STANDARD; PRT; 537 AA.
AC 010269;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable sterol O-acetyltransferase (EC 2.3.1.26) (Sterol-ester
synthase).
GN SPAC137.05.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetes; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Frazer A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsle K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grynolprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabbel C., Fuchs M., Filtz C., Holzer E., Moesli D., Hilbert H.,
 RA Borzom P., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambolt R., Punnett B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaurie V., Mortier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Roche M., Galliard C., Talada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Carrutti L., Lowe T., McCombie W.R., Paulsen I., Poteskin J.,
 RA Sipakavski G.V., Usery D., Barrett B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*,"
 RT Nature 415:871-880(2002).
 CC -1- CATALYTIC ACTIVITY: Acyl-CoA + cholesterol = CoA + cholesterol
 CC ester.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: Z69729; CA93593.1; -.
 CC PIR: S67434; S67434.
 DR GeneDB: Spombe; SPAC1367.05; -.
 DR Pfam: PF03062; MBOAT_1.
 KW Hypothetical protein; Transferrase; Transmembrane;
 KW Endoplasmic reticulum; Acyltransferase.
 FT TRANSMEM 140 118 POTENTIAL.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 305 325 POTENTIAL.
 FT TRANSMEM 344 364 POTENTIAL.
 FT TRANSMEM 384 404 POTENTIAL.
 FT TRANSMEM 482 482 POTENTIAL.
 FT TRANSMEM 488 508 POTENTIAL.
 FT TRANSMEM 517 537 POTENTIAL.
 FT CARBOHYD 250 250 POTENTIAL.
 SQ SEQUENCE 537 AA; 63098 MW; 41DBA79402B67A28 CRC64; (POTENTIAL).
 QY Query Match 62.3%; Score 38; DB 1; Length 537;
 Best Local Similarity 58.3%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 PLSISFRIQDP 12
 DB 79 PRKSIFDRTDP 90
 RESULT 12
 UVRB CHLTR STANDARD; PRT; 1786 AA.
 AC 084337;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE UVRAC system protein A (UvrA protein) (Exonuclease ABC subunit A).
 GN UVRB OR CT333.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/UW-3/Cx;
 RX MEDLINE=99000809; PubMed=9784136.
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatunov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;

RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.";
 RT Science 282:754-759(1998).
 CC -1- FUNCTION: The UvrABC repair system catalyzes the recognition and
 CC processing of DNA lesions. UvrA is an ATPase and a DNA-binding
 CC protein. A damage recognition complex composed of 2 uvrA and 2
 CC uvrB subunits scans DNA for abnormalities. When the presence of a
 CC lesion has been verified by uvrB, the uvrA molecules dissociate
 CC (By similarity).
 CC -1- SUBUNIT: Forms a heterotrimer with uvrB during the search for
 CC lesions (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRB SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AE001306; AAC67928.1; -.
 CC PIR: H71527; H71527.
 DR HAMAP: MF_00205; -; 2.
 DR InterPro: IPR003439; ABC transporter.
 DR InterPro: IPR004602; UvrA.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transporter; 1.
 DR TIGRfam: TIGR00630; UvrA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
 DR PROSITE: PS50893; ABC_TRANSPORTER_2; 2.
 KW SOS response; Excision nuclease; DNA repair; DNA recombination;
 KW DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
 KW Zinc-finger; Complete proteome.
 FT NP_BIND 32 39 ATP (POTENTIAL).
 FT NP_BIND 625 632 ATP (POTENTIAL).
 FT ZN_FING 719 742 C4-TYPE.
 FT NP_BIND 964 971 ATP (POTENTIAL).
 FT NP_BIND 1516 1523 ATP (POTENTIAL).
 FT ZN_FING 1602 1628 C4-TYPE.
 SQ SEQUENCE 1786 AA; 196948 MW; 02D6862EE15DE070 CRC64;
 QY Query Match 62.3%; Score 38; DB 1; Length 1786;
 Best Local Similarity 63.6%; Pred. No. 63;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LSSISFRIQDP 12
 DB 1042 LESLFTRIQHP 1052
 RESULT 13
 YOR2 CAEBL STANDARD; PRT; 495 AA.
 AC 009307;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 45.1 kDa protein F19C6.2 in chromosome X.
 GN F19C6.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Harris B.;
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
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DR EMBL; 248006; CNA8050.1; -
DR PIR; T2115; T2115.
DR WormPep; F19C6.2; CE032231.
KW Hypothetical protein.
SQ SEQUENCE 495 AA; 55814 MW; 99EB952032B0B48C CRC64;

Query Match 60.7%; Score 37; DB 1; Length 495;
Best Local Similarity 45.5%; Pred. No. 26;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PUSISFRIGD 11
Db 278 PVSGLFQKVD 288

RESULT 14
MWIN SYN3 STANDARD; PRT; 533 AA.
AC 055179;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Virulence factor mvin homolog.
GN MWIN OR SLR0488.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneo T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 644 to 924 of the genome.";
RL DNA Ref. 2:153-166(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE MWIN FAMILY.
CC
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EMBL; D64001; BAA10319.1; -
DR PIR; S74401.
DR InterPro; IPR004268; MWIN_1like.
DR Pfam; PF03023; MWIN; 1.
KW Transmembrane, Complete proteome.

FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 96 116 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
FT TRANSMEM 253 273 POTENTIAL.
FT TRANSMEM 284 304 POTENTIAL.
FT TRANSMEM 330 350 POTENTIAL.
FT TRANSMEM 360 380 POTENTIAL.
FT TRANSMEM 400 420 POTENTIAL.
FT TRANSMEM 422 442 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
FT TRANSMEM 493 513 POTENTIAL.
SQ SEQUENCE 533 AA; 57053 MW; 00ASB612F744CID2 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 533;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PUSISFRIGDP 12
Db 300 PFLPVFSRLADP 311

RESULT 15
S2IG_HUMAN STANDARD; PRT; 848 AA.
ID S2IG_HUMAN
AC 09H2Y9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Solute carrier family 21 member 15 (Organic anion transporter
DE polypeptide-related protein 4) (OATP-RP4) (OATP4).
GN SLC21A15.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu Y., Heiang B.H., Zhu Y., Yang W.-P., Kirchgessner T.G.;
RT "Identification and characterization of novel human OATP family
RT members.";
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RL -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS.

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EMBL; AF205075; AAG42207.1; -
DR Genew; HGNC:19046; SLC21A15.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR004157; OATP_Cterm.
DR InterPro; IPR004156; OATP_Nterm.
DR Pfam; PF03137; OATP_C; 1.
DR Pfam; PF03132; OATP_N; 1.
DR TIGRPAWS; TIGR00805; oat; 1.
KW Transmembrane; Transport; Glycoprotein.
FT TRANSMEM 129 149 POTENTIAL.
FT TRANSMEM 168 188 POTENTIAL.
FT TRANSMEM 198 218 POTENTIAL.
FT TRANSMEM 261 281 POTENTIAL.
FT TRANSMEM 304 324 POTENTIAL.
FT TRANSMEM 348 368 POTENTIAL.
FT TRANSMEM 435 455 POTENTIAL.
FT TRANSMEM 473 493 POTENTIAL.
FT TRANSMEM 506 526 POTENTIAL.
FT TRANSMEM 651 671 POTENTIAL.
FT TRANSMEM 696 716 POTENTIAL.
FT TRANSMEM 736 756 POTENTIAL.
FT DOMAIN 377 383 POLY-LYS.
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 550 550 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 597 597 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 730 730 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQL SEQUENCE 848 AA; 91877 MW; F7BDC260744B7FA4 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 848;

Best Local Similarity 50.0%; Pred. No. 45;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLSSIFSRIGDP 12

DB 776 PLSTVSERVGHF 787

RESULT 16

DCUP_CHLMU STANDARD; PRT; 334 AA.

AC 09PLHT;

DT 16-OCT-2001 (Rel. 40, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).

GN HEME OR TC0123.

OS Chlamydia muridarum.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_Taxid=33560;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MOPN / N199;

RA MEDLINE=20150255; PubMed=10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

White O., Hickey E.K., Peterson J., Uetzerback T., Berry K., Bass S.,

Linher K., Weidman J., Khouri H., Craven B., Bowman R.,

RA Gaim M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,

Eisen J., Fraser C.M.,

RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia

pneumoniae AR39."

RL Nucleic Acids Res. 28:1397-1406(2000).

CC -1- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4

CC CO(2).

CC -1- PATHWAY: Porphyrin biosynthesis.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -1- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.

CC -----

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CC -----

CC EMBL; AE002279; AAF39001.1; -

DR PIR; F81739; F81739.

DR HSSP; P06133; URO.

DR TIGR; TC0123; -

DR HAMAP; MF_00218; -; 1.

DR InterPro; IPR006361; Heme.

DR InterPro; IPR000257; Uro_decarboxyls.

DR Pfam; PF01208; URO-D; 1.

DR ProDom; PD003225; Uro_decarboxyls; 1.

DR TIGRFAMs; TIGR01464; Heme; 1.

DR PROSITE; PS00906; UROD_1; 1.

DR PROSITE; PS00907; UROD_2; 1.

DR Lyase; Decarboxylase; Porphyrin biosynthesis; Complete proteome.

SQL SEQUENCE 334 AA; 37380 MW; 199BA88AC1F4DD CRC64;

Query Match 59.0%; Score 36; DB 1; Length 334;

Best Local Similarity 54.5%; Pred. No. 26;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12

DB 258 LSEIYRQLGDP 268

RESULT 17

WMSA_HPBVM STANDARD; PRT; 369 AA.

AC P03172;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Major surface antigen precursor.

GN S.

OS Hepatitis B virus (subtype adw).

OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_Taxid=106821;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83168919; PubMed=6300776;

RA Ono Y., Ono H., Sasada R., Igarashi K., Sugino Y., Nishioka K.,

RT "The complete nucleotide sequences of the cloned hepatitis B virus

RT DNA; subtype adr and adw."

RL Nucleic Acids Res. 11:1747-1757(1983).

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CC -----

CC EMBL; V00866; CA24233.1; ALT_INIT.

DR PIR; A93460; SALVE.

DR InterPro; IPR000349; Hepvir_surfag.

DR Pfam; PF00695; WMSA; 1.

KM Antigen.

FT PROPP 1 163

FT CHAIN 164 389

FT CARBOHYD 4 4

FT CARBOHYD 26 26

FT CARBOHYD 112 112

FT CARBOHYD 166 166

FT CARBOHYD 309 309

SQL SEQUENCE 389 AA; 42354 MW; FB9EF27BEFC5B5 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 389;

Best Local Similarity 63.6%; Pred. No. 31;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12

DB 150 ISSISARTGDP 160

RESULT 18

WMSA_HPBVM STANDARD; PRT; 400 AA.

ID WMSA_HPBVM

AC P03141;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Major surface antigen precursor.

GN S.

OS Hepatitis B virus (subtype adw2).

OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_Taxid=10408;

RN [1]

RP SEQUENCE FROM N.A.

RA Valenzuela P., Zaldívar J., Gray P., Rutter W.J.,

RL (in) Field B.N., Jaenisch R., Fox C.F. (eds.);

RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).

RN [2]

RP SEQUENCE OF 175-400 FROM N.A.

RX MEDLINE=79244739; PubMed=471053;

RA Valenzuela P., Gray P., Zaldívar J., Goodman H.M.,

RA Rutter W.J.;

RT "Nucleotide sequence of the gene coding for the major protein of
RT hepatitis B virus surface antigen.";
RL Nature 280:815-819 (1979).
CC -----
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CC -----
CC EMBL; X02763; CAA26539.1; -
DR EMBL; J02205; AAA4524.1; -
DR PIR; A03706; SAVLYD.
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
KW PROPEP.
FT CHAIN 1 174 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 15 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43704 MW; 57356B6293872BC5 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 400;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
Db 161 ISSISARTGDP 171

RESULT 19
VMSA HPBV9 STANDARD; PRT; 400 AA.
ID VMSA HPBV9
AC P17101;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain 991).
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koehnel H.G., Schneller A., Lotmann S., Thomassen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBD databases.
CC -----
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CC -----
CC EMBL; X51970; CAA36230.1; -
DR PIR; S10383; SAVLKS.
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
KW PROPEP.
FT CHAIN 1 174 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 15 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43695 MW; 76D98F74B8B17724 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 400;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
Db 161 ISSISARTGDP 171

RESULT 20
MP44_MCV1 STANDARD; PRT; 593 AA.
ID MP44_MCV1
AC Q98224; O11329;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable metalloendopeptidase Gl-type (EC 3.4.24.-).
GN MC056L OR B2'-17R.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96325459; PubMed=8670425;
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RT "Genome sequence of a human tumorigenic poxvirus: prediction of
RT specific host response-evasion genes.";
RL Science 273:813-816 (1996).
RN [2]
RP SEQUENCE OF 206-392 FROM N.A.
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
RA Lopez-Bestebaranz J.L., Esteban M., Martin-Gallardo A.;
RT "A random DNA sequencing, computer-based approach for the
RT generation of a gene map of Molluscum Contagiosum virus.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBD databases.
CC -1- FUNCTION: Seems to be involved in viral proteins maturation by
CC cleavage at Ala-Gly-|-Xaa motifs (by similarity).
CC -1- COFACTOR: BINDS 1 ZINC ION (Potential).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M44.
CC -----
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CC -----
CC EMBL; U60315; AAC55184.1; -
DR EMBL; U66909; AAB57961.1; -
DR PIR; T30658; T30658.
DR MEROPS; M44.001; -
DR InterPro; IPR005072; Peptidase_M44.
DR Pfam; PF03410; Peptidase_M44; 1.
KW Hydrolase; Metalloprotease; Zinc.
FT METAL 41 41 ZINC (CATALYTIC) (POTENTIAL).
FT ACT SITE 44 44 ZINC (CATALYTIC) (POTENTIAL).
FT METAL 45 45 ZINC (CATALYTIC) (POTENTIAL).
SQ SEQUENCE 593 AA; 68419 MW; 142C620E1AB0C61B CRC64;

Query Match 59.0%; Score 36; DB 1; Length 593;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12
Db 381 PRAEYFVRIGDP 392

RESULT 21
EPGL_SYNY3

ID EFG1_S1YX3 STANDARD; PRT; 695 AA.
AC P28371; P74556;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G 1 (EF-G 1).
GN FUS1 OR FUS OR SLR1463.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
RX MEDLINE=94339485; PubMed=8061323;
RA Melisch P.L., Johnson D., Zhang Y., Breitenberger C.A.;
RT "Synechocystis sp. PCC6803 ftsB gene, located outside of the str
operon, encodes a polypeptide related to protein synthesis factor
EF-G.";
RL Plant Mol. Biol. 25:735-738 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
RA Osouchi T., Matsuno A., Muraki A., Nakazaki N., Natsu K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136 (1996).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION
OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC -----
CC EMBL; X65159; CAA46277.1; -;
DR EMBL; D90916; BAI18663.1; -;
DR PIR; S76751; S76751.
DR HSP; P13551; 2EFG.
DR HAMAP; MF_00054; -; 1.
DR InterPro; IPR004540; EF-G.
DR InterPro; IPR000795; EF GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFCCT.
DR TIGRfams; TIGR00484; EF-G; 1.
DR TIGRfams; TIGR00231; small_GTP; 1.
DR PROSITE; PS00301; EFATOR_GTP; 1.
KW Elongation factor; protein biosynthesis; GTP-binding;
KW Multigene family; Complete proteome.
FT NE_BIND 15 22 GTP (BY SIMILARITY).
FT NE_BIND 79 83 GTP (BY SIMILARITY).
FT NE_BIND 133 136 GTP (BY SIMILARITY).
FT CONFICT 42 42 H->R (IN REF. 1).
SQ SEQUENCE 695 AA; 76750 MW; 8727830BP9073223 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 695;

Best Local Similarity 63.6%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 PLSSIFSRIGD 11
DB 645 PLSMFYIGD 655
RESULT 22
EFG_MICLU STANDARD; PRT; 701 AA.
AC P09352;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G).
GN FUS1 OR FUS.
OS Micrococcus luteus (Micrococcus lysodeikticus).
OC Bacteria; Actinobacteria; Actinomycetales;
OC Micrococcales; Micrococcaceae; Micrococcus.
NCBI_TaxID=1270;
RX MEDLINE=88007427; PubMed=3654584;
RA Ohama T., Yamao F., Muto A., Osawa S.;
RT "Organization and codon usage of the streptomycin operon in
Micrococcus luteus, a bacterium with a high genomic G + C content.";
RL J. Bacteriol. 169:4770-4777 (1987).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION
OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC -----
CC EMBL; M17788; AAA25319.1; -;
DR PIR; C26956; C26956.
DR HSP; P13551; 1DAR.
DR HAMAP; MF_00054; -; 1.
DR InterPro; IPR004540; EF-G.
DR InterPro; IPR000795; EF GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFCCT.
DR TIGRfams; TIGR00484; EF-G; 1.
DR TIGRfams; TIGR00231; small_GTP; 1.
DR PROSITE; PS00301; EFATOR_GTP; 1.
KW Elongation factor; protein biosynthesis; GTP-binding;
FT NE_BIND 15 22 GTP (BY SIMILARITY).
FT NE_BIND 79 83 GTP (BY SIMILARITY).
FT NE_BIND 133 136 GTP (BY SIMILARITY).
SQ SEQUENCE 701 AA; 77425 MW; 25E49FACF350E236 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 701;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 PLSSIFSRIGD 11

Db 655 PUSEMFGYIGD 665

RESULT 23

MUTS_VIRCH STANDARD; PRT; 862 AA.

AC 09K016;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE DNA mismatch repair protein muts.
 GN MUTS OR VC0535.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxId=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RL Nature 406:477-483(2000).
 CC -1- FUNCTION: This protein is involved in the repair of mismatches in
 DNA. It is possible that it carries out the mismatch recognition
 step. This protein has a weak ATPase activity (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL; AE004139; AAF93703.1; -
 CC TIGR; VC0535; -
 DR HAMAP; MF_00096; -; 1.
 DR InterPro; IPR005748; MutS1.
 DR InterPro; IPR000432; MutS_C.
 DR InterPro; IPR007860; MutS_II.
 DR InterPro; IPR007696; MutS_III.
 DR InterPro; IPR007861; MutS_IV.
 DR InterPro; IPR007695; MutS_N.
 DR Pfam; PF01624; MutS_1; 1.
 DR Pfam; PF05188; MutS_II; 1.
 DR Pfam; PF05192; MutS_III; 1.
 DR Pfam; PF05190; MutS_IV; 1.
 DR Pfam; PR00488; MutS_V; 1.
 DR ProDom; PD001263; MutS_C; 1.
 DR SMART; SM00534; Mutsac; 1.
 DR SMART; SM00533; Mutsd; 1.
 DR TIGRfam; TIGR01070; muts1; 1.
 DR PROSITE; PS00486; DNA_MISMATCH_REPAIR_2; 1.
 DR DNA repair; ATP-binding; DNA-binding; Complete proteome.
 KW NP_BIND 621 628 ATP (POTENTIAL).
 FT SEQUENCE 862 AA; 96326 MW; 98882509B7140531 CRC64;
 SQ

Query Match 59.0%; Score 36; DB 1; Length 862;
 Best Local Similarity 70.0%; Pred. No. 70;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PUSIFSRIG 10
 DB 656 PLDIRIFTRIG 665

RESULT 24

PDR6_YEAST STANDARD; PRT; 1081 AA.

AC P32767;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE pleiotropic drug resistance regulatory protein 6.
 GN PDR6 OR KAP122 OR YGL016W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL125-2B;
 RX MEDLINE=91353083; PubMed=1882553;
 RA Chen W., Balzi E., Capleau E., Choder M., Goffeau A.;
 RT "The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1
 and ATR1 loci on chromosome VII from Saccharomyces cerevisiae reveals
 the PDR6 gene, a new member of the genetic network controlling
 pleiotropic drug resistance.";
 RT Yeast 7:287-299(1991).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Hedling U., Hofmann B., Delius H.;
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLE POSITIVE REGULATOR OF PROTEINS INVOLVED IN
 PERMEABILITY.
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 CC EMBL; S58126; AADI3901.1; -
 CC EMBL; S57895; AABI9613.1; -
 CC EMBL; Z72538; CAA96716.1; -
 DR PIR; S15040; S15040.
 DR SCD; S0002984; KAP122.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005643; C:nuclear pore; IDA.
 DR GO; GO:0006006; P:protein-nucleus import; IDA.
 SQ SEQUENCE 1081 AA; 123530 MW; EBBCSADD4E16D9D3 CRC64;
 SQ

Query Match 59.0%; Score 36; DB 1; Length 1081;
 Best Local Similarity 63.6%; Pred. No. 89;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LSIFSRIGD 12
 DB 118 LSLIFTKINDP 128

RESULT 25

EFG_STRRA STANDARD; PRT; 341 AA.

AC P29541;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G) (Fragment).
 GN FUS.
 OS Streptomyces ramocissimus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxId=1925;
 RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=9428341; PubMed=8012612;
RA Vajgenboom E., Woudt L.P., Heinstra P.W.H., Rietveld K.,
RT "Three tuf-like genes in the kitomycin producer Streptomyces
RT ramocissimus.";
RL Microbiology 140:983-998(1994).
CC -1- FUNCTION. THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC -----
DR EMBL; X67057; CAA47441.1; -.
DR PIR; S23907; S23907.
DR HSSP; P13551; IELO.
DR HAMAP; MF_00054; -.
DR InterPro; IPR000795; IPR_GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PROSITE; PS00301; EFATOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON TER 1
SQ SEQUENCE 341 AA; 37322 MW; DEEDC72A0A62F91 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 341;
Best Local Similarity 54.5%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PLSISFRIGDP 11
Db 295 PLSMFVGVGD 305

RESULT 26
VMSA_HPBVI STANDARD; PRT; 389 AA.
ID VMSA_HPBVI STANDARD; PRT; 389 AA.
AC P17397;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S
OS Hepatitis B virus (subtype adw / strain Indonesia/PTM420).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10412;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Saetosewignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
CC -----
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CC -----
DR EMBL; D00331; -. NOT_ANNOTATED_CDS.
DR PIR; I28925; SAVLJ3.
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 163
FT CHAIN 164 389
FT CARBOHYD 4 4
FT CARBOHYD 112 112
FT CARBOHYD 166 166
FT CARBOHYD 309 309
SQ SEQUENCE 389 AA; 42653 MW; 08079BA34F3B9C0 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 389;
Best Local Similarity 63.6%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LSSIFSRIGDP 12
Db 150 ISSILSTGDP 160

RESULT 27
VMSA_HPBVT STANDARD; PRT; 400 AA.
ID VMSA_HPBVT STANDARD; PRT; 400 AA.
AC Q05496;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=54410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93346970; PubMed=8345355;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4.";
RL J. Gen. Virol. 74:1627-1632(1993).
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CC -----
DR EMBL; X69798; CAA49455.1; -.
DR PIR; J02230; J02230.
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174
FT CHAIN 175 400
SQ SEQUENCE 400 AA; 43551 MW; 4A5A2212E4B3E117 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 400;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSIFSRIGDP 12
Db 162 SSIFSRIGDP 171

RESULT 28

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IPGD_SHIFL STANDARD; PRT; 538 AA.
ID IPGD_SHIFL
AC Q07566; Q8VSH4;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE IPGD protein.
GN IPGD OR CP0133.
OS Shigella flexneri.
OC Plasmid pWR100, and Plasmid pCP301.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_Taxid=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / Serotype 5; PLASMID=pWR100;
RX MEDLINE=93239268; PubMed8478058;
RA Allouat A., Menard R., Sansonetti P.J., Parrot C.;
RT "Characterization of the Shigella flexneri ipgd and ipgf genes, which
are located in the proximal part of the mxi locus.";
RL Infect. Immun. 61:1707-1714(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / Serotype 5; PLASMID=pWR100;
RX MEDLINE=20566792; PubMed1115111;
RA Buchrieser C., Glaeser P., Rusnok C., Nedjari H., d'Hauteville H.,
Kunat F., Sansonetti P., Parrot C.;
RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
by the type III secretion apparatus of Shigella flexneri.";
RL Mol. Microbiol. 38:760-771(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / Serotype 5; PLASMID=pWR100;
RX MEDLINE=21189246; PubMed11292750;
RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
Blattner F.R.;
RT "Complete DNA sequence and analysis of the large virulence plasmid of
Shigella flexneri.";
RL Infect. Immun. 69:3271-3285(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a; PLASMID=pCP301;
RX MEDLINE=22272406; PubMed12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu D., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -----
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CC -----
CC EMBL, L04309; AAA26517.1; -
CC EMBL, AL391753; CAC05808.1; -
CC DR EMBL, AF348706; AKI8452.1; -
CC DR EMBL, AF36526; AAL72339.1; -
CC -----
CC Virulence; Plasmid.
KM VARIANT 73 73 K -> R (IN PLASMID PCP301).
FT VARIANT 155 155 N -> D (IN PLASMID PCP301).
FT VARIANT 166 166 S -> G (IN PLASMID PCP301).
FT VARIANT 200 200 R -> S (IN PLASMID PCP301).
FT VARIANT 300 300 S -> N (IN PLASMID PCP301).
FT VARIANT 311 311 G -> E (IN PLASMID PCP301).
FT VARIANT 406 406 NN -> TK (IN PLASMID PCP301).
FT VARIANT 424 424 V -> M (IN PLASMID PCP301).

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SQ SEQUENCE 538 AA; 59832 MW; 304D27839C64CF96 CRC64;
Query Match
Best Local Similarity 57.4%; Score 35; DB 1; Length 538;
Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
QY 1 PLSST-----FSRIGDP 12
DB 510 PLSSTLSYSERIGDP 525
RESULT 29
EFG MYCLE STANDARD; PRT; 701 AA.
ID EFG_MYCLE
AC P30767;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G).
GN FUS4 OR EFG OR ML1878.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1769;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188701; PubMed8446028;
RA Honore N.T., Bergh S., Chanteau S., Doucet-Populaire F.,
Eigmeier K., Garnier T., Georges C., Lannots P., Limpitpon T.,
RA Newton S., Niang K., del Portillo P., Ramesh G.R., Reddi P.,
RA Ridel P.R., Sittisombut N., Wu-Hunter S., Cole S.T.;
RT "Nucleotide sequence of the first cosmid from the Mycobacterium
leprae genome project: structure and function of the Rif-str
regions.";
RL Mol. Microbiol. 7:207-214(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornby T., Jagsels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skellon J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -----
CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC -----
CC EMBL, Z14314; CAA78673.1; -
CC DR EMBL, AL583923; CAC30832.1; -
CC DR PIR, H87143; H87143.
CC PIR, S31150; S31150.
CC HSRP, P13551; IEFNM.
CC Leproma; ML1878; -.
CC DR HAMAP, MF_00054; -.
CC DR InterPro, IPR004540; EF-G.

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DR InterPro: IPR000795; EF-GTPbind.
DR InterPro: IPR000640; EFG_C.
DR InterPro: IPR005517; EFG_IV.
DR InterPro: IPR004161; EFTU_D2.
DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00679; EFG_C; 1.
DR Pfam: PF03764; EFG_IV; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR PRINTS: PRO0315; ELONGATNFCR.
DR TIGRPFAM: TIGR00484; EF-G; 1.
DR TIGRPFAM: TIGR00231; small_GTP; 1.
DR PROSITE: PS00301; EFACITOR GTP; 1.
KM Elongation factor: Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP_BIND 20 27 GTP (BY SIMILARITY).
FT NP_BIND 84 88 GTP (BY SIMILARITY).
FT NP_BIND 138 141 GTP (BY SIMILARITY).
FT CONFLICT 564 564 G -> A (IN REF. 1).
SQ SEQUENCE 701 AA; 77160 MW; F18B724F35F3181E CRC64;

Query Match 57.4%; Score 35; DB 1; Length 701;
Best Local Similarity 54.5%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PLSSIFSRIGD 11
DB 655 PLSMFGYVD 665

RESULT 30
EFG_MYCTU STANDARD; PRT; 701 AA.
AC 053790;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G).
GN FUSA OR RV0684 OR MT0712 OR MT040.12 OR MTCV210.01.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultsen J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Petersen J., DeBoy R., Dodson R., Gwinn M.L., Hatt D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Orntoft L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Uitterlind T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
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CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AL021943; CAI17471.1; -
CC EMBL: AE006965; AA44938.1; -
CC PIR: E70827; E70827.
CC HSSP: P13551; 1FNM.
CC TIGR: MT0712; -.
DR Tuberculosis; RV0684; -.
DR HAMAP: MF_00054; -.
DR InterPro: IPR004540; EF-G.
DR InterPro: IPR000795; EF-GTPbind.
DR InterPro: IPR000640; EFG_C.
DR InterPro: IPR005517; EFG_IV.
DR InterPro: IPR004161; EFTU_D2.
DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00679; EFG_C; 1.
DR Pfam: PF03764; EFG_IV; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR PRINTS: PRO0315; ELONGATNFCR.
DR TIGRPFAM: TIGR00484; EF-G; 1.
DR TIGRPFAM: TIGR00231; small_GTP; 1.
DR PROSITE: PS00301; EFACITOR GTP; 1.
KM Elongation factor: Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP_BIND 20 27 GTP (BY SIMILARITY).
FT NP_BIND 84 88 GTP (BY SIMILARITY).
FT NP_BIND 138 141 GTP (BY SIMILARITY).
SQ SEQUENCE 701 AA; 77202 MW; 0CEDD4C128E31E1A1 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 701;
Best Local Similarity 54.5%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PLSSIFSRIGD 11
DB 655 PLSMFGYVD 665

RESULT 31
EFG_CORGL STANDARD; PRT; 705 AA.
AC 08NT19;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G).
GN FUSA OR CGJ0495.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
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CC -----
CC EMBL, AP005275; BAB97888.1; -.
CC HAMAP, MF_00054; -.
CC InterPro: IPR004540; EF-G.
CC InterPro: IPR000795; EF_GTPbind.
CC InterPro: IPR000640; EFG_C.
CC InterPro: IPR005517; EFG_IV.
CC InterPro: IPR004161; EFTU_D2.
CC InterPro: IPR005225; Small_GTP.
CC Pfam; PF00679; EFG_C; 1.
CC Pfam; PF03764; EFG_IV; 1.
CC Pfam; PF00009; GTP_EFTU; 1.
CC Pfam; PF03144; GTP_EFTU_D2; 1.
CC PRINTS; PRO0315; ELONGATNFCT.
CC TIGRfams; TIGR00484; EF-G; 1.
CC TIGRfams; TIGR00231; small_GTP; 1.
CC PROSITE; PS00301; EFACITOR_GTP; 1.
CC Elongation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP_BIND 15 22 GTP (BY SIMILARITY).
FT NP_BIND 79 83 GTP (BY SIMILARITY).
FT NP_BIND 133 136 GTP (BY SIMILARITY).
SQ SEQUENCE 705 AA; 77464 MW; 6CD7010C4110B2F2 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 705;
Best Local Similarity 54.5%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PLSSTFSRIGD 11
DB 657 PLSQMFQYVGD 667

RESULT 32
EFG1_STRCO STANDARD; PRT; 708 AA.
AC PA0173; OSLOK3;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G 1 (EF-G 1).
GN FUS1 OR FUS OR SCO4661 OR SCO4604.07.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kisser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser T., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kisser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)";
RL Nature 417:141-147(2002).
RN [2]
RP SEQUENCE OF 616-708 FROM N.A.
RC STRAIN=A3(2) / M145;

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RX MEDLINE=95002174; PubMed=7918656;
RA van Wezel G.P., Moud L.P., Verweene R., Verdunmen M.L.,
RA Vijgenboom E., Bosch L.;
RT "Cloning and sequencing of the tuf genes of Streptomyces coelicolor
RT A3(2)";
RL Biochim. Biophys. Acta 1219:543-547(1994).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC -----
CC EMBL, AL939121; CAB81852.1; -.
CC EMBL, X77039; CA54328.1; -.
CC PIR, S50137; S50137.
CC HSSP; P13551; 1DAR.
CC HAMAP, MF_00054; -.
CC InterPro: IPR004540; EF-G.
CC InterPro: IPR000795; EF_GTPbind.
CC InterPro: IPR000640; EFG_C.
CC InterPro: IPR005517; EFG_IV.
CC InterPro: IPR004161; EFTU_D2.
CC InterPro: IPR005225; Small_GTP.
CC Pfam; PF00679; EFG_C; 1.
CC Pfam; PF03764; EFG_IV; 1.
CC Pfam; PF00009; GTP_EFTU; 1.
CC Pfam; PF03144; GTP_EFTU_D2; 1.
CC PRINTS; PRO0315; ELONGATNFCT.
CC TIGRfams; TIGR00484; EF-G; 1.
CC TIGRfams; TIGR00231; small_GTP; 1.
CC PROSITE; PS00301; EFACITOR_GTP; 1.
CC Elongation factor; Protein biosynthesis; GTP-binding;
KW Multigene family; Complete proteome.
FT NP_BIND 18 25 GTP (BY SIMILARITY).
FT NP_BIND 86 90 GTP (BY SIMILARITY).
FT NP_BIND 140 143 GTP (BY SIMILARITY).
SQ SEQUENCE 708 AA; 77657 MW; 3660298061D3B1B CRC64;

Query Match 57.4%; Score 35; DB 1; Length 708;
Best Local Similarity 54.5%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 PLSSTFSRIGD 11
DB 662 PLSQMFQYVGD 672

RESULT 33
RRPL_BTIV10 STANDARD; PRT; 1302 AA.
AC P13840;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (VP1).
GN S1.
OS Bluetongue virus (serotype 10 / isolate USA).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=10900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89098323; PubMed=2850542;
RX Roy P., Fukusho A., Ritter G.D., Lyon D.;
RT "Evidence for genetic relationship between RNA and DNA viruses from

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RT the sequence homology of a putative polymerase gene of bluetongue
RT virus with that of vaccinia virus: conservation of RNA polymerase
RT genes from diverse species.";
RL Nucleic Acids Res. 16:11759-11767(1988).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE=90345726; PubMed=2166648;
RA Roy P., Marshall J.J.A., French T.J.;
RT "Structure of the bluetongue virus genome and its encoded proteins.";
RL Curr. Top. Microbiol. Immunol. 162:43-87(1990).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -----
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CC -----
DR EMBL; X12819; CAA31306.1; -.
DR PIR; A34296; REXRST.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007097; RNA_pol_rec.
DR Transference; Nucleotidyltransferase: RNA-directed RNA polymerase.
SQ SEQUENCE 1302 AA; 149586 MW; 0C063AE396FC3D CRC64;

Query Match 57.4%; Score 35; DB 1; Length 1302;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLSIFSRIG 10
DB 539 PLSIFSRVWG 548

RESULT 34
NUSG_LIBAS
ID NUSG_LIBAS STANDARD; PRT; 70 AA.
AC P36262;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription antitermination protein nusg (fragment).
GN NUSG.
OS Liberibacter asiaticus (Liberobacter asiaticum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX Rhizobiaceae; Candidatus Liberibacter.
RX NCB1_TaxID=34021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93153297; PubMed=7763375;
RA Vilcheanoux S., Garnier M., Laryret F., Renaudin J., Bove J.M.;
RT "The genome of the non-cultured, bacterial-like organism associated
RT with citrus greening disease contains the nusg-rp1kxJL-rp0bC gene
RT cluster and the gene for a bacteriophage type DNA polymerase.";
RL Curr. Microbiol. 26:161-166(1992).
CC -1- FUNCTION: INFLUENCES TRANSCRIPTION TERMINATION AND
CC ANTITERMINATION. ACTS AS A COMPONENT OF THE TRANSCRIPTION COMPLEX,
CC AND INTERACTS WITH THE TERMINATION FACTOR RHO AND RNA POLYMERASE
CC (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the nusg family.
CC -----
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CC -----
DR EMBL; M94319; AAA23104.1; -.

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DR InterPro; IPR005824; KOW.
DR InterPro; IPR006646; KOW sub.
DR InterPro; IPR001062; NusG.
DR Pfam; PF00467; KOW; 1.
DR SMART; SM00739; KOW; 1.
DR PROSITE; PS01014; NUSG; 1.
KW Transcription termination.
FT NON TER 1
SQ SEQUENCE 70 AA; 7749 MW; 563C62DB9A0C485 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 70;
Best Local Similarity 45.5%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLSIFSRIGD 11
DB 10 PLSVFFEVGE 20

RESULT 35
NTCA_SYNY3
ID NTCA_SYNY3 STANDARD; PRT; 225 AA.
AC P33779;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Global nitrogen regulator.
GN NTCA OR SL1423.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCB1_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93374871; PubMed=8366058;
RA Frias J.E., Merida A., Herrero A., Martin-Nieto J.M., Flores E.;
RT "General distribution of the nitrogen control gene ntca in
RT cyanobacteria.";
RL J. Bacteriol. 175:5710-5713(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Saito S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: REQUIRED FOR FULL EXPRESSION OF PROTEINS SUBJECT TO
CC AMMONIUM REPRESSION. TRANSCRIPTIONAL ACTIVATOR OF GENES SUBJECT TO
CC NITROGEN CONTROL.
CC -1- SIMILARITY: BELONGS TO THE CRP/FNR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
DR EMBL; X71607; CAA50607.1; -.
DR EMBL; D90911; BAA18011.1; -.
DR PIR; A48640; A48640.
DR InterPro; IPR000595; cNMP binding.
DR InterPro; IPR001808; HTH_Crp.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00325; Crp; 1.
DR PRINTS; PR00034; HTHCRP.
DR SMART; SM00100; cNMP; 1.

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DR SMART; SM00419; HTH CRP; 1.
 DR PROSITE; PS00042; HTH CRP FAMILY; 1.
 DR PROSITE; PS00042; CNAME BINDING 3; 1.
 KW Transcription regulation; DNA-binding; Activator; Complete proteome.
 FT NP BIND 9 131 CNAME.
 FT DNA BIND 177 196 H-T-H MOTIF (BY SIMILARITY).
 SQ SEQUENCE 225 AA; 25046 MW; F1EB6555757E7379 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 225;
 Best Local Similarity 50.0%; Pred. No. 42;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLSIFSRIG 10
 Db 10 PLAAVRRRLG 19

RESULT 36
 YGFF_ECOLI STANDARD; PRT; 247 AA.

ID YGFF_ECOLI STANDARD; PRT; 247 AA.
 AC P52037; P71138; Q46830;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase ygfF (EC 1.1.1.1).
 GN YGFF OR B2902.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12";
 RL Science 277:1453-1474 (1997).

[2]
 SEQUENCE OF 1-74 FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE=94162733; PubMed=7764507;
 RA Yamada M., Yanai S., Talkner A.;
 RT "Analysis of products of the Escherichia coli genomic genes and
 RT regulation of their expressions: an applicable procedure for genomic
 RT analysis of other microorganisms";
 RL Biosci. Biotechnol. Biochem. 58:117-120 (1994).
 RN [3]
 RP SEQUENCE OF 137-197 FROM N.A.

RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
 RA Duncan M., Federpriel N., Hyman R., Kaiman S., Komp C., Kurdi O.,
 RA Lew H., Lin D., Namach A., Oefner P., Schramm S., Davis R.W.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; U28377; AAA69070.1; -
 CC EMBL; U28375; AAA63083.1; -
 CC EMBL; AE000373; AAC75940.1; -
 CC EMBL; D21144; BAA04680.1; -
 CC EMBL; U83189; AAB40290.1; -
 CC PIR; F65074; F65074.
 DR HSP; P19992; IHDC.

DR Ecogene; EG12971; ygfF.
 DR InterPro; IPR002198; ADH short.
 DR Pfam; PF0106; adh short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; Complete proteome.
 FT NP BIND 4 28
 FT ACT SITE 156 156 NAD OR NADP (BY SIMILARITY).
 FT ACT SITE 156 156 BY SIMILARITY.
 SQ SEQUENCE 247 AA; 25938 MW; 8F17257B5905E4F9 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 247;
 Best Local Similarity 54.5%; Pred. No. 46;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LLSIFSRIGDP 12
 Db 140 VSSVASRLGSP 150

RESULT 37
 VGLL_HSV6Z

ID VGLL_HSV6Z STANDARD; PRT; 250 AA.
 AC P52526;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glycoprotein L precursor.
 GN GL OR U82 OR CB10L.
 GN Human herpesvirus (type 6 / strain 229) (HHV6).
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Roseolovirus.
 OX NCBI_TaxID=36351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96195263; PubMed=8634027;
 RX Lindquester G.J., Inoue N., Allen R.D., Castelli J.W.,
 RA Stamey F.R., Dambaugh T.R., O'Brian J.J., Danovich R.M.,
 RA Frenkel N., Pellett P.E.;
 RT "Restriction endonuclease mapping and molecular cloning of the human
 RT herpesvirus 6 variant B strain 229 genome";
 RL Arch. Virol. 141:367-379 (1996).
 CC -1- FUNCTION: ASSOCIATED WITH GLYCOPROTEIN H (GH) TO FORM A COMPLEX
 CC IMPORTANT FOR INFECTION AND CELL FUSION.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN L.

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CC EMBL; AF157706; AAB06366.1; -
 CC PIR; T44227; T44227.
 DR InterPro; IPR002689; Cytomegalin GL.
 DR Pfam; PF01801; Cytomegalin GL; 1.
 KW Glycoprotein; Signal.

FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 250 GLYCOPROTEIN L.
 FT CARBOHYD 41 41 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 250 AA; 28903 MW; 0ED7723F5019A104 CRC64;

Query Match 55.7%; Score 34; DB 1; Length 250;
 Best Local Similarity 54.5%; Pred. No. 47;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LLSIFSRIGDP 12
 Db 101 LRTLFALIGDP 111

RESULT 38
NMA HUMAN
ID NMA HUMAN STANDARD; PRT; 260 AA.
AC Q13145;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Putative transmembrane protein NMA precursor.
GN NMA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96184146; PubMed=8621228;
RA Degen W.G.U., Wettermann M.A., van Groningen J.J.M.,
RA Cornelissen I.M.A.H., Lemmers J.P.W.M., Agterbos M.A.,
RA van Kessel A.G., Swart G.W.M., Bloemers H.P.J.;
RT "Expression of nma, a novel gene, inversely correlates with the
RT metastatic potential of human melanoma cell lines and xenografts.";
RN Int. J. Cancer 65:460-465(1996).
[2]
RP SEQUENCE FROM N.A.
RA Pearce A.;
RN Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RN MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
RA Altschuld S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko U., Marziani K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Cantinici P., Pirange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Baskin S.A., McKernan P.J., McKernan K.J., Malek J.A., Gamarale P.H.,
RA Richarde S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN KIDNEY MEDULLA, PLACENTA
CC AND SPLEEN; LOW IN KIDNEY CORTEX, LIVER, PROSTATE AND GUT. NOT
CC EXPRESSED IN NORMAL SKIN. EXPRESSION IS HIGH IN MELANOCYTES AND IN
CC 3 OUT OF 11 MELANOMA METASTASES TESTED.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IN POORLY METASTATIC HUMAN
CC MELANOMA CELL LINES; NO EXPRESSION IN HIGHLY METASTATIC HUMAN
CC MELANOMA CELL LINES.
CC -----
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CC -----
CC EMBL: U23070; AAC50435.1; -;
CC EMBL: AL161936; CAC16002.1; -;
CC EMBL: BC019252; AAH19252.1; -;
CC MIM: 604444; -;
CC DR GO: GO:0016021; C: integral to membrane; TAS.
CC DR GO: GO:0007048; P: oncogenesis; TAS.

KW Transmembrane; Signal; Glycoprotein.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 260 PUTATIVE TRANSMEMBRANE PROTEIN NMA.
FT TRANSMEM 153 173 POTENTIAL.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 260 AA; 29107 MW; 70C2326883858AB CRC64;
Query Match
Best Local Similarity 55.7%; Score 34; DB 1; Length 260;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LSISFRIGDP 12
DB 48 LSACFSRLDP 58
RESULT 39
CB23 TOBAC
ID CB23 TOBAC STANDARD; PRT; 265 AA.
AC P27494;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chlorophyll A-B binding protein 36, chloroplast precursor (LHCII type
DE I CAB-36) (LHCP).
GN CAB36.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. Havana.
RC Kavanagh T.A., Bevan M.W.;
RN Submitted (MAR-1991) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT
RECEPTOR, IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS
WITH WHICH IT IS CLOSELY ASSOCIATED. THE N-TERMINUS OF THE PROTEIN
EXTENDS INTO THE STROMA WHERE IT IS INVOLVED WITH ADHESION OF
GRAVIL MEMBRANES AND PHOTOREGULATED BY REVERSIBLE PHOSPHORYLATION
OF ITS THREONINE RESIDUES; BOTH ARE BELIEVED TO MEDIATE THE
DISTRIBUTION OF EXCITATION ENERGY BETWEEN PHOTOSYSTEMS I AND II.
CC -1- SUBUNIT: THE LHC COMPLEX CONSISTS OF CHLOROPHYLLS (A & B) AND
CC CHLOROPHYLL A-B BINDING PROTEINS.
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -----
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CC -----
CC EMBL: X58230; CAA41188.1; -;
CC PIR: S21827; S21827.
DR InterPro: IPR001344; Chloro_Abbind.
DR Pfam: PF00504; chloro_a-b-bind; 1.
DR ProDom: PD000275; Chloro_Abbind; 1.
KW Chlorophyll; Photosynthesis; Photosystem I; Photosystem II;
KW Thylakoid; Membrane; Chloroplast; Transic peptide; Multigene family;
KW Transmembrane; Phosphorylation.
FT TRANSIT 1 36 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 37 265 CHLOROPHYLL A-B BINDING PROTEIN 36.
SQ SEQUENCE 265 AA; 28638 MW; C9A2B59A84F5A8E4 CRC64;
Query Match
Best Local Similarity 33.3%; Pred. No. 50;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 PLUSIFSRIGDP 12

Db 238 PIENLFDHVADP 249

RESULT 40

CE23_HORVU

ID CB23_HORVU STANDARD; PRT; 268 AA.

AC P27523;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chlorophyll A-B binding protein of LHClI type III, chloroplast

DE precursor (CAB).

GN LHCB.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;

OC Triticeae; Hordeum.

OC NCBI_TaxID=4513;

OK [1]

RN SEQUENCE FROM N.A.

RP STRAIN=cv. Pallas / P-01;

RX MEDLINE=92329730; PubMed=1627782;

RA Brandt J., Nielsen V.S., Thordal-Christensen H., Simpson D.J.,

Okels J.S.;

RT "A barley cDNA clone encoding a type III chlorophyll a/b-binding

polypeptide of the light-harvesting complex II.";

RL Plant Mol. Biol. 19:699-703(1992).

CC -! FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT

RECEPTOR, IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS

WITH WHICH IT IS CLOSELY ASSOCIATED. THE N-TERMINUS OF THE PROTEIN

EXTENDS INTO THE STROMA WHERE IT IS INVOLVED WITH ADHESION OF

GRANAL MEMBRANES AND PHOTOREGULATED BY REVERSIBLE PHOSPHORYLATION

OF ITS THREONINE RESIDUES; BOTH ARE BELIEVED TO MEDIATE THE

DISTRIBUTION OF EXCITATION ENERGY BETWEEN PHOTOSYSTEMS I AND II.

CC -! SUBUNIT: THE LHC COMPLEX CONSISTS OF CHLOROPHYLLS (A & B) AND

CHLOROPHYLL A-B BINDING PROTEINS.

CC -! SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.

CC -----

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CC -----

DR EMBL; X63197; CAA44881.1; -.

DR PIR; S22482; CDBH3.

DR InterPro; IPR001344; Chloro_Abbind.

DR Pfam; PF00504; chloro_a_b_bind; 1.

DR ProDom; PD000275; Chloro_Abbind; 1.

KM Chlorophyll; Photosynthesis; Photosystem II; Thylakoid; Membrane;

KW Chloroplast; Transit peptide; Multigene family; Transmembrane;

KW Phosphorylation.

FT TRANSIT 1 45

FT CHAIN 1 45

FT TRANSIT 1 45

FT CHAIN 1 45

FT TRANSIT 1 45

FT CHAIN 1 45

FT TRANSIT 1 45

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FT CHAIN 1 45

FT TRANSIT 1 45

FT CHAIN 1 45

FT TRANSIT 1 45

FT CHAIN 1 45

FT TRANSIT 1 45

FT CHAIN 1 45

Query Match 55.7%; Score 34; DB 1; Length 268;
Best Local Similarity 41.7%; Pred. No. 50;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 PLSIFSRIGDP 12

DB 241 PIENLFDHDDP 252

Search completed: November 6, 2003, 15:11:54
Job time : 12 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2003, 15:09:04 ; Search time 34 Seconds
(without alignments)
91.077 Million cell updates/sec

Title: US-09-830-981-2
Perfect score: 61
Sequence: 1 PLSIFSRIGDP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	57	12 Q91IC1	Q91IC1 hepatitis b
2	61	100.0	163	12 Q9WP19	Q9WP19 hepatitis b
3	61	100.0	281	12 Q41750	Q41750 hepatitis b
4	61	100.0	281	12 Q8QXP8	Q8QXP8 hepatitis b
5	61	100.0	378	12 Q67944	Q67944 hepatitis b
6	61	100.0	378	12 Q67954	Q67954 hepatitis b
7	61	100.0	383	12 Q96837	Q96837 hepatitis b
8	61	100.0	383	12 Q96840	Q96840 hepatitis b
9	61	100.0	389	12 Q8QXP9	Q8QXP9 hepatitis b
10	61	100.0	389	12 Q67875	Q67875 hepatitis b
11	61	100.0	389	12 Q9WMX3	Q9WMX3 hepatitis b
12	61	100.0	389	12 Q91CS5	Q91CS5 hepatitis b
13	61	100.0	389	12 Q90772	Q90772 hepatitis b
14	61	100.0	389	12 Q91CS2	Q91CS2 hepatitis b
15	59	96.7	49	12 Q91IC3	Q91IC3 hepatitis b
16	59	96.7	55	12 Q91XP4	Q91XP4 hepatitis b

17	59	96.7	55	12 Q91X62	Q91X62 hepatitis b
18	59	96.7	55	12 Q91XD1	Q91XD1 hepatitis b
19	59	96.7	55	12 Q91X89	Q91X89 hepatitis b
20	59	96.7	55	12 Q91XD0	Q91XD0 hepatitis b
21	59	96.7	55	12 Q91XA3	Q91XA3 hepatitis b
22	59	96.7	55	12 Q91X64	Q91X64 hepatitis b
23	59	96.7	55	12 Q91X83	Q91X83 hepatitis b
24	59	96.7	55	12 Q91XA1	Q91XA1 hepatitis b
25	59	96.7	55	12 Q91X86	Q91X86 hepatitis b
26	59	96.7	55	12 Q91X92	Q91X92 hepatitis b
27	59	96.7	55	12 Q91X76	Q91X76 hepatitis b
28	59	96.7	55	12 Q91XA0	Q91XA0 hepatitis b
29	59	96.7	55	12 Q91XC2	Q91XC2 hepatitis b
30	59	96.7	55	12 Q91XE9	Q91XE9 hepatitis b
31	59	96.7	55	12 Q91XB0	Q91XB0 hepatitis b
32	59	96.7	55	12 Q91XB3	Q91XB3 hepatitis b
33	59	96.7	55	12 Q91XB6	Q91XB6 hepatitis b
34	59	96.7	55	12 Q91X98	Q91X98 hepatitis b
35	59	96.7	55	12 Q91X65	Q91X65 hepatitis b
36	59	96.7	55	12 Q91XF2	Q91XF2 hepatitis b
37	59	96.7	55	12 Q91XB5	Q91XB5 hepatitis b
38	59	96.7	55	12 Q91XD9	Q91XD9 hepatitis b
39	59	96.7	55	12 Q91XA9	Q91XA9 hepatitis b
40	59	96.7	55	12 Q91X74	Q91X74 hepatitis b
41	59	96.7	55	12 Q91XD4	Q91XD4 hepatitis b
42	59	96.7	55	12 Q91X94	Q91X94 hepatitis b
43	59	96.7	55	12 Q91XC7	Q91XC7 hepatitis b
44	59	96.7	55	12 Q91X88	Q91X88 hepatitis b
45	59	96.7	55	12 Q91XC5	Q91XC5 hepatitis b

ALIGNMENTS

RESULT 1
Q91IC1 PRELIMINARY; PRT; 57 AA.
ID Q91IC1
AC Q91IC1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Pre-S2 protein (Major surface antigen) (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N314-1;
RA Huangfu J., Deng J., Deng H.;
RT "Preliminary Study on Pres2 Region of Hepatitis B Virus";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF393223; AAK64362.1; -;
DR InterPro; IPR00349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
KW Non_Ter.
FT NON_TER.
SQ SEQUENCE 57 AA; 6124 MW; 8D756AF55FF849CF CRC64;
Query Match 100.0%; Score 61; DB 12; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLSIFSRIGDP 12
DB 41 PLSIFSRIGDP 52
RESULT 2
ID Q9WP19 PRELIMINARY; PRT; 163 AA.
AC Q9WP19;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
DE Large S protein (Major surface antigen) (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MF;
RT "Kidd-Ljunggren K.;
RT "Nosocomial Transmission of Hepatitis B Virus Through Multiple Dose
RT "Vials.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF136461; AAD44711.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 163 AA; 17331 MW; 38020BE460F0BD24 CRC64;
Query Match 100.0%; Score 61; DB 12; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
DB 149 PLSSTFSRIGDP 160

RESULT 3

ID 041750 PRELIMINARY; PRT; 281 AA.
AC 041750;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
DE Middle S protein (Major surface antigen).
GN PRES2/S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=E08;
RX MEDLINE=97368435; PubMed=9225049;
RA Bower S., van Staden L., Kew M.C., Sim J.G.;
RT "A unique segment of the hepatitis B virus group A genotype identified
RT in isolates from South Africa."
RL EMBL; U87737; AAC58018.1; -
RL J. Gen. Virol. 78:1719-1729(1997).
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 281 AA; 31153 MW; 85D90E7B5F2C9289 CRC64;

QY Query Match 100.0%; Score 61; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
DB 41 PLSSTFSRIGDP 52

RESULT 4

ID 080XP8 PRELIMINARY; PRT; 281 AA.
AC 080XP8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
DE Middle surface antigen (Major surface antigen).
GN PRES2.
RT Hepatitis B virus.

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN (1)
RP SEQUENCE FROM N.A.
RA Kay A.C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Jeanter D., Chemin I., Mandrand B., Zoulim F., Trepo C., Kay A.;
RT "Characterization of two Hepatitis B virus populations isolated from a
RT Hepatitis B surface antigen-negative patient."
RL Hepatology 0:0-0(0).
DR EMBL; AJ344117; CAC87014.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 281 AA; 31266 MW; 37234BBD949B3B03 CRC64;

QY Query Match 100.0%; Score 61; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
DB 41 PLSSTFSRIGDP 52

RESULT 5

ID 067944 PRELIMINARY; PRT; 378 AA.
AC 067944;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
DE Surface proteins (Major surface antigen).
GN PRES1/PRES2.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN (1)
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Portu A., Balestrieri A.;
RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85254; CAA59510.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 378 AA; 41257 MW; D4370B06FFB625D5 CRC64;

QY Query Match 100.0%; Score 61; DB 12; Length 378;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSSTFSRIGDP 12
DB 149 PLSSTFSRIGDP 160

RESULT 6

ID 067954 PRELIMINARY; PRT; 378 AA.
AC 067954;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
DE HBV surface proteins (Major surface antigen) (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN (1)
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Balestrieri A.;
RT "Sequence analysis of HBV genomes isolated from patients with HBsAg

RT Chronic liver disease."
 RL Submitted (JAN-1994) to the EMBL/Genbank/DBJ databases.
 DR EMBL; X77309; CAA54515.1; -
 DR InterPro; IPR000349; Hepvir_surfAg.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 FT NON_TER
 SQ SEQUENCE 378 AA; 41356 MW; FCI8839606E121CD CRC64;

Query Match 100.0%; Score 61; DB 12; Length 378;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
 |||||
 Db 149 PLSIFSRIGDP 160

RESULT 7
 Q96837 PRELIMINARY; PRT; 383 AA.
 AC Q96837.
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Large S protein (Major surface antigen) (Fragment).
 GN PRE-S/S.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BH;
 RX MEDLINE=97049068; PubMed=8893798;
 RA Moraes M.T., Gomes S.A., Niel C.;
 RT "Sequence analysis of pre-S/S gene of hepatitis B virus strains of
 RT genotypes A, D, and F isolated in Brazil."
 RL Arch. Virol. 141:1767-1773(1996).
 DR EMBL; U55224; AAB47470.1; -
 DR InterPro; IPR000349; Hepvir_surfAg.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 FT NON_TER
 SQ SEQUENCE 383 AA; 41942 MW; 6E10F3B7471B6B1 CRC64;

Query Match 100.0%; Score 61; DB 12; Length 383;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
 |||||
 Db 149 PLSIFSRIGDP 160

RESULT 8
 Q96840 PRELIMINARY; PRT; 383 AA.
 AC Q96840.
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Large S protein (Major surface antigen) (Fragment).
 GN PRE-S/S.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BKJ;
 RX MEDLINE=97049068; PubMed=8893798;
 RA Moraes M.T., Gomes S.A., Niel C.;
 RT "Sequence analysis of pre-S/S gene of hepatitis B virus strains of
 RT genotypes A, D, and F isolated in Brazil."

RL Arch. Virol. 141:1767-1773(1996).
 DR EMBL; U55227; AAB47473.1; -
 DR InterPro; IPR000349; Hepvir_surfAg.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 FT NON_TER
 SQ SEQUENCE 383 AA; 42018 MW; 341AB53B7911BBDC CRC64;

Query Match 100.0%; Score 61; DB 12; Length 383;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
 |||||
 Db 149 PLSIFSRIGDP 160

RESULT 9
 Q80XP9 PRELIMINARY; PRT; 389 AA.
 AC Q80XP9.
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Large surface antigen (Major surface antigen).
 GN PRE-S1.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kay A.C.;
 RT Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jeanter D., Chemin I., Mandrand B., Zoulim F., Trepo C., Kay A.;
 RT "Characterization of two Hepatitis B virus populations isolated from a
 RT Hepatitis B surface antigen-negative patient."
 RL Hepatology 0:0-0(0).
 DR EMBL; AJ344117; CAC87013.1; -
 DR InterPro; IPR000349; Hepvir_surfAg.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 SQ SEQUENCE 389 AA; 42764 MW; 9AC5A4D46B73632 CRC64;

Query Match 100.0%; Score 61; DB 12; Length 389;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIGDP 12
 |||||
 Db 149 PLSIFSRIGDP 160

RESULT 10
 Q67875 PRELIMINARY; PRT; 389 AA.
 AC Q67875.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Pre S1/S ORF (Major surface antigen).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lai M.E., Mazzioleni A.P., Balestrieri A., Mellis A., Porru A.;
 RT "Sequence analysis of HBV genomes isolated from patients with HBsAg
 RT negative chronic liver disease."
 RL Submitted (MAR-1992) to the EMBL/Genbank/DBJ databases.
 DR EMBL; X65258; CAA46353.1; -
 DR InterPro; IPR000349; Hepvir_surfAg.

DR Pfam: PF00695; VMSA; 1.
KM Antigen.
SQ SEQUENCE 389 AA; 42661 MW; A39542B416A6F24 CRC64;
Query Match 100.0%; Score 61; DB 12; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PLSSIFSRIGDP 12
Db 149 PLSSIFSRIGDP 160
RESULT 11
Q9WMX3 PRELIMINARY; PRT; 389 AA.
ID Q9WMX3
AC Q9WMX3;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RA MEDLINE=99238050; PubMed10223539;
RA Petrol D.R.; Tautz B.; Wolf F.; Drescher J.;
RT "Infection chains and evolution rates of Hepatitis B Virus in cardiac
transplant recipients infected nosocomially.";
RL J. Med. Virol. 58:1-10 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RA Petrol D.R.;
RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ131956; CAA10540.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KM Antigen.
FT CHAIN 164 389 SURFACE ANTIGEN.
SQ SEQUENCE 389 AA; 42708 MW; 6AA08B85DFE5B99C CRC64;
Query Match 100.0%; Score 61; DB 12; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PLSSIFSRIGDP 12
Db 149 PLSSIFSRIGDP 160
RESULT 12
Q91C55 PRELIMINARY; PRT; 389 AA.
ID Q91C55
AC Q91C55;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Large/middle/small S proteins (Major surface antigen).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RA MEDLINE=21361467; PubMed11468728;
RA Owiredu W.K.; Kramvis A.; Kew M.C.;
RT "Hepatitis B virus DNA in serum of healthy black African adults
positive for hepatitis B surface antibody alone: possible association
with recombination between genotypes A and D.";

RL J. Med. Virol. 64:441-454 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RA Owiredu W.K.B.A.; Kramvis A.; Kew M.C.;
RT Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF297619; AAK97179.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KM Antigen.
SQ SEQUENCE 389 AA; 42580 MW; F4336E04992CE6E2 CRC64;
Query Match 100.0%; Score 61; DB 12; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PLSSIFSRIGDP 12
Db 149 PLSSIFSRIGDP 160
RESULT 13
Q90772 PRELIMINARY; PRT; 389 AA.
ID Q90772
AC Q90772;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Surface protein (Major surface antigen).
GN S GENE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ref2;
RA MEDLINE=98362187; PubMed9696878;
RA Grethe S.; Monazahian M.; Boehme I.; Thomssen R.;
RT "Characterization of unusual escape variants of hepatitis B virus
isolated from a hepatitis B surface antigen-negative subject.";
RL J. Virol. 72:7692-7696 (1998).
DR EMBL; AJ003116; CAA05872.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KM Antigen.
SQ SEQUENCE 389 AA; 42682 MW; 575E7223D068CDB CRC64;
Query Match 100.0%; Score 61; DB 12; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PLSSIFSRIGDP 12
Db 149 PLSSIFSRIGDP 160
RESULT 14
Q91C52 PRELIMINARY; PRT; 389 AA.
ID Q91C52
AC Q91C52;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Large/middle/small S proteins (Major surface antigen).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=57;
RA MEDLINE=21361467; PubMed11468728;
RA Owiredu W.K.; Kramvis A.; Kew M.C.;
RT "Hepatitis B virus DNA in serum of healthy black African adults

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RA Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
RT molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL/ AF247933; AAF62188.1; -.
DR InterPro: IPR000349; Hepvir_surfg.
DR Pfam; PF00695; vWSA; 1.
KW Antigen.
KW Antigen.
FT NON TER
FT NON TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSISFRIQDP 12
|:|||||
|:|||||
Db 41 PISISFRIQDP 52

RESULT 17
O91X62 PRELIMINARY; PRT; 55 AA.
AC O91X62.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE PreS2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam18;
RX MEDLINE=20440648; PubMed=10970376;
RA Flogdren B., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
RA Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
RT molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247963; AAF62276.1; -.
DR InterPro: IPR000349; Hepvir_surfg.
DR Pfam; PF00695; vWSA; 1.
KW Antigen.
KW Antigen.
FT NON TER
FT NON TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSISFRIQDP 12
|:|||||
|:|||||
Db 41 PISISFRIQDP 52

RESULT 18
O91XD1 PRELIMINARY; PRT; 55 AA.
ID O91XD1
AC O91XD1.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE PreS2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam18;

```

RX MEDLINE=20440648; PubMed=10970376;
 RA Ploggren E., Bengtsson S., Knutsson M., Strebbkova E.A., Kidd A.H.,
 RA Alexeyev O.A., Kidd-Ljunggren K.;
 RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
 RT molecular analysis of prevailing hepatitis B and D virus strains.";
 RL J. Clin. Microbiol. 38:3311-3316(2000).
 DR EMBL; AF247940; AAF62207.1; -
 DR InterPro; IPR000349; Hepvit_surfAg.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT NON_TER
 SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match 96.7%; Score 59; DB 12; Length 55;
 Best Local Similarity 91.7%; Pred. No. 0.00084;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFSTRIGDP 12
 Db 41 PLSISFSTRIGDP 52

RESULT 19

Q91X89 PRELIMINARY; PRT; 55 AA.
 AC Q91X89;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Pres1 protein (Major surface antigen) (Fragment).
 GN S.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_Taxid=10407;
 RX MEDLINE=20440648; PubMed=10970376;
 RC STRAIN=Sam77;
 RP SEQUENCE FROM N.A.
 RA Ploggren E., Bengtsson S., Knutsson M., Strebbkova E.A., Kidd A.H.,
 RA Alexeyev O.A., Kidd-Ljunggren K.;
 RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
 RT molecular analysis of prevailing hepatitis B and D virus strains.";
 RL J. Clin. Microbiol. 38:3311-3316(2000).
 DR EMBL; AF247954; AAF62249.1; -
 DR InterPro; IPR000349; Hepvit_surfAg.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT NON_TER
 SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match 96.7%; Score 59; DB 12; Length 55;
 Best Local Similarity 91.7%; Pred. No. 0.00084;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFSTRIGDP 12
 Db 41 PLSISFSTRIGDP 52

RESULT 20

Q91XD0 PRELIMINARY; PRT; 55 AA.
 AC Q91XD0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Pres1 protein (Major surface antigen) (Fragment).
 GN S.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_Taxid=10407;
 RP SEQUENCE FROM N.A.

RC STRAIN=Sam33;
 RX MEDLINE=20440648; PubMed=10970376;
 RA Ploggren E., Bengtsson S., Knutsson M., Strebbkova E.A., Kidd A.H.,
 RA Alexeyev O.A., Kidd-Ljunggren K.;
 RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
 RT molecular analysis of prevailing hepatitis B and D virus strains.";
 RL J. Clin. Microbiol. 38:3311-3316(2000).
 DR EMBL; AF247941; AAF62212.1; -
 DR InterPro; IPR000349; Hepvit_surfAg.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT NON_TER
 SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match 96.7%; Score 59; DB 12; Length 55;
 Best Local Similarity 91.7%; Pred. No. 0.00084;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFSTRIGDP 12
 Db 41 PLSISFSTRIGDP 52

RESULT 21

Q91XA3 PRELIMINARY; PRT; 55 AA.
 AC Q91XA3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Pres1 protein (Major surface antigen) (Fragment).
 GN S.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_Taxid=10407;
 RX MEDLINE=20440648; PubMed=10970376;
 RC STRAIN=Sam65;
 RP SEQUENCE FROM N.A.
 RA Ploggren E., Bengtsson S., Knutsson M., Strebbkova E.A., Kidd A.H.,
 RA Alexeyev O.A., Kidd-Ljunggren K.;
 RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
 RT molecular analysis of prevailing hepatitis B and D virus strains.";
 RL J. Clin. Microbiol. 38:3311-3316(2000).
 DR EMBL; AF247950; AAF62239.1; -
 DR InterPro; IPR000349; Hepvit_surfAg.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT NON_TER
 SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match 96.7%; Score 59; DB 12; Length 55;
 Best Local Similarity 91.7%; Pred. No. 0.00084;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLSISFSTRIGDP 12
 Db 41 PLSISFSTRIGDP 52

RESULT 22

Q91X64 PRELIMINARY; PRT; 55 AA.
 AC Q91X64;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Pres1 protein (Major surface antigen) (Fragment).
 GN S.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

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OX NCB1_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam128;
RX MEDLINE=20440648; PubMed=10970376;
RA Floodgren E., Bengtsson S., Knutsson M., Strebekova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247963; AAF62278.1; -
DR InterPro; IPR000349; Hepvit_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match 96.7%; Score 59; DB 12; Length 55;
Best Local Similarity 91.7%; Pred. No. 0.00084;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSIFSRIGDP 12
   |:::|||||
Db 41 PLSIFSRIGDP 52

RESULT 23
Oy 091X83 PRELIMINARY; PRT; 55 AA.
ID 091X83
AC 091X83;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam93;
RX MEDLINE=20440648; PubMed=10970376;
RA Floodgren E., Bengtsson S., Knutsson M., Strebekova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247956; AAF62255.1; -
DR InterPro; IPR000349; Hepvit_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match 96.7%; Score 59; DB 12; Length 55;
Best Local Similarity 91.7%; Pred. No. 0.00084;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSIFSRIGDP 12
   |:::|||||
Db 41 PLSIFSRIGDP 52

RESULT 24
Oy 091X1 PRELIMINARY; PRT; 55 AA.
ID 091X1
AC 091X1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
```

```

OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam65;
RX MEDLINE=20440648; PubMed=10970376;
RA Floodgren E., Bengtsson S., Knutsson M., Strebekova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247950; AAF62237.1; -
DR InterPro; IPR000349; Hepvit_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match 96.7%; Score 59; DB 12; Length 55;
Best Local Similarity 91.7%; Pred. No. 0.00084;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSIFSRIGDP 12
   |:::|||||
Db 41 PLSIFSRIGDP 52

RESULT 25
Oy 091X86 PRELIMINARY; PRT; 55 AA.
ID 091X86
AC 091X86;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCB1_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam82;
RX MEDLINE=20440648; PubMed=10970376;
RA Floodgren E., Bengtsson S., Knutsson M., Strebekova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247955; AAF62252.1; -
DR InterPro; IPR000349; Hepvit_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match 96.7%; Score 59; DB 12; Length 55;
Best Local Similarity 91.7%; Pred. No. 0.00084;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PLSIFSRIGDP 12
   |:::|||||
Db 41 PLSIFSRIGDP 52

RESULT 26
Oy 091X92 PRELIMINARY; PRT; 55 AA.
ID 091X92
AC 091X92;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
```

GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_Taxid=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam76;
RX MEDLINE=20440648; PubMed=10970376;
RA Flogdren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:"
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247953; AAF62246.1; -
DR InterPro; IPR000349; Hepvit_surflag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFSTRIGDP 12
Db 41 PLSISFSTRIGDP 52

RESULT 27
Q9IX76 PRELIMINARY; PRT; 55 AA.
AC Q9IX76;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Pres1 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_Taxid=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam104;
RX MEDLINE=20440648; PubMed=10970376;
RA Flogdren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:"
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247959; AAF62266.1; -
DR InterPro; IPR000349; Hepvit_surflag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFSTRIGDP 12
Db 41 PLSISFSTRIGDP 52

RESULT 28
Q9IXA0 PRELIMINARY; PRT; 55 AA.
AC Q9IXA0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Pres1 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_Taxid=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam68;
RX MEDLINE=20440648; PubMed=10970376;
RA Flogdren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:"
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247951; AAF62242.1; -
DR InterPro; IPR000349; Hepvit_surflag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON TER
SQ SEQUENCE 55 AA; 5892 MW; 4AB600FC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFSTRIGDP 12
Db 41 PLSISFSTRIGDP 52

RESULT 29
Q9IXC2 PRELIMINARY; PRT; 55 AA.
AC Q9IXC2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_Taxid=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam38;
RX MEDLINE=20440648; PubMed=10970376;
RA Flogdren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:"
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247943; AAF62216.1; -
DR InterPro; IPR000349; Hepvit_surflag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFSTRIGDP 12
Db 41 PLSISFSTRIGDP 52

RESULT 30
Q9IXE9 PRELIMINARY; PRT; 55 AA.
AC Q9IXE9;


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DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam9;
RX MEDLINE=20440648; PubMed=10970376;
RA Floodgren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247934; AAF62189.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFSTRIGDP 12
Db 41 PLSISFSTRIGDP 52

RESULT 31
Q91XB0 PRELIMINARY; PRT; 55 AA.
ID Q91XB0;
AC Q91XB0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam58;
RX MEDLINE=20440648; PubMed=10970376;
RA Floodgren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247947; AAF62228.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFSTRIGDP 12
Db 41 PLSISFSTRIGDP 52

RESULT 32
Q91XB3 PRELIMINARY; PRT; 55 AA.
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AC Q91XB3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam52;
RX MEDLINE=20440648; PubMed=10970376;
RA Floodgren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247946; AAF62225.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFSTRIGDP 12
Db 41 PLSISFSTRIGDP 52

RESULT 33
Q91XB6 PRELIMINARY; PRT; 55 AA.
ID Q91XB6;
AC Q91XB6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam12;
RX MEDLINE=20440648; PubMed=10970376;
RA Floodgren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247935; AAF62192.1; -
DR InterPro; IPR000349; Hepvir_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSISFSTRIGDP 12
Db 41 PLSISFSTRIGDP 52

RESULT 34
Q91XB8
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ID Q9IX98 PRELIMINARY; PRT; 55 AA.
AC Q9IX98;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam68;
RX MEDLINE=20440648; PubMed=10970376;
RA Floegren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.,
  "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RT J. Clin. Microbiol. 38:3311-3316(2000).
RL EMBL: AF247951; AAF62240.1; -
DR InterPro: IPR000349; Hepvit_surflAg.
DR Pfam: PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5892 MW; 4AB600FC488BF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PLSISFSRIGDP 12
Db 41 PLSISFSRIGDP 52

RESULT 35
O9IX65 PRELIMINARY; PRT; 55 AA.
ID Q9IX65;
AC Q9IX65;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam125;
RX MEDLINE=20440648; PubMed=10970376;
RA Floegren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.,
  "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RT J. Clin. Microbiol. 38:3311-3316(2000).
RL EMBL: AF247962; AAF62273.1; -
DR InterPro: IPR000349; Hepvit_surflAg.
DR Pfam: PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PLSISFSRIGDP 12
Db 41 PLSISFSRIGDP 52

RESULT 36
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O9IXF2 PRELIMINARY; PRT; 55 AA.
ID Q9IXF2;
AC Q9IXF2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam7;
RX MEDLINE=20440648; PubMed=10970376;
RA Floegren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.,
  "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RT J. Clin. Microbiol. 38:3311-3316(2000).
RL EMBL: AF247933; AAF62186.1; -
DR InterPro: IPR000349; Hepvit_surflAg.
DR Pfam: PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PLSISFSRIGDP 12
Db 41 PLSISFSRIGDP 52

RESULT 37
O9IXB5 PRELIMINARY; PRT; 55 AA.
ID Q9IXB5;
AC Q9IXB5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Pres1 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam52;
RX MEDLINE=20440648; PubMed=10970376;
RA Floegren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
  Alexeyev O.A., Kidd-Ljunggren K.,
  "Recent high incidence of fulminant hepatitis in Samara, Russia:
  molecular analysis of prevailing hepatitis B and D virus strains.";
RT J. Clin. Microbiol. 38:3311-3316(2000).
RL EMBL: AF247946; AAF62227.1; -
DR InterPro: IPR000349; Hepvit_surflAg.
DR Pfam: PF00695; VMSA; 1.
KW Antigen.
FT NON_TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PLSISFSRIGDP 12
Db 41 PLSISFSRIGDP 52
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RESULT 38
Q9IXD9 PRELIMINARY; PRT; 55 AA.
AC Q9IXD9;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Pres1 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam15;
RX MEDLINE=20440648; PubMed=10970376;
RA Plodgren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
RA Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
RT molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247938; AAF62203.1; -
DR InterPro; IPR000349; Hepvit_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON TER
FT NON TER
SQ SEQUENCE 55 AA; 5892 MW; 52514FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIQDP 12
Db 41 PLSIFSRIQDP 52

RESULT 39
Q9IXA9 PRELIMINARY; PRT; 55 AA.
AC Q9IXA9;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Pres1 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam59;
RX MEDLINE=20440648; PubMed=10970376;
RA Plodgren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
RA Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
RT molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247948; AAF62233.1; -
DR InterPro; IPR000349; Hepvit_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON TER
FT NON TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIQDP 12
Db 41 PLSIFSRIQDP 52

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIQDP 12

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Db 41 PLSIFSRIQDP 52

RESULT 40
Q9IX74 PRELIMINARY; PRT; 55 AA.
AC Q9IX74;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Pres2 protein (Major surface antigen) (Fragment).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sam104;
RX MEDLINE=20440648; PubMed=10970376;
RA Plodgren E., Bengtsson S., Knutsson M., Strebkova E.A., Kidd A.H.,
RA Alexeyev O.A., Kidd-Ljunggren K.;
RT "Recent high incidence of fulminant hepatitis in Samara, Russia:
RT molecular analysis of prevailing hepatitis B and D virus strains.";
RL J. Clin. Microbiol. 38:3311-3316(2000).
DR EMBL; AF247959; AAF62264.1; -
DR InterPro; IPR000349; Hepvit_surfAg.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON TER
FT NON TER
SQ SEQUENCE 55 AA; 5863 MW; 4AB61FEC488BFF73 CRC64;

Query Match
Best Local Similarity 96.7%; Score 59; DB 12; Length 55;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSIFSRIQDP 12
Db 41 PLSIFSRIQDP 52

Search completed: November 6, 2003, 15:12:42
Job time : 36 secs

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